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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	Run on: March 24, 2004, 21:53:36; Search time 508.584 Seconds (without alignments) 1960.127 Million cell updates/sec	Title: US-09-889-611A-19 Perfect score: 23 Sequence: 1 gaatgaactacataacaaccacc 23	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 3470272 seqs, 21671516995 residues	Total number of hits satisfying chosen parameters: 6940544	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	1. gb htg:* 2: gb htg:* 4: gb_on:* 4: gb_on:* 5: gb pov:* 6: gb pov:* 7: gb_pi:* 10: gb_ov:* 11: gb_bi:* 10: gb_ov:* 11: gb_bi:* 11: gb_si:* 11: gb_ov:* 11: gb_ov:* 11: gb_ov:* 11: gb_ov:* 12: gb_ov:* 13: gb_ov:* 13: gb_ov:* 14: gb_ov:* 15: gb_ov:* 16: gb_ov:* 17: gb_ov:* 18: gb_ov:* 18: gb_ov:* 19: gb_ov:* 10: gb_ov		
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

TITLE JOURNAL

AUTHORS JOURNAL

REFERENCE

AUTHORS

REFERENCE

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Direct Submission

All Submitted (25-NOV-201) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 157284)

8 sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, M., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, W., Dawar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gader, D., Galagan, J., Gardyna, S., Gond, S., Govette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, J., Levine, R., Liuf, G., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liuf, G., Marchis, C., Macchand, P., McCarth, M., McEwan, P., McGarnan, R., Marquis, N., Matthews, C., Macchand, P., Major, J., Nguyen, C., Macchand, P., McGarth, M., McDwan, P., McGarnan, R., Narphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Connell, P., 
                                                                    Birren, S.C. Challes Oliver, Camulinger, in Mills, Allen, N., Barren, S.C. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, Y., Camarata, J., Camarata, A., Collins, S., Collymore, A., Cook, A., Cooke, Y., Devar, K., Dewar, K., Diang, J., S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, I., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, I., Gardyna, S., Ginde, S., Gord, S., Karatas, A., Kalls, C., Lakocque, K., Landers, T., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Maran, C.H., McGarnan, K., McPheeters, R., Meldrim, J., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Comnor, T., O'Nonnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roetta, R., Palamas, J., Tesfaye, S., Theodore, J., Sewery, P., Spencer, B., Schauer, S., Schubar, S., Severy, P., Spencer, B., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wiman, D., Ye, W.J., Young, G., Nimithe, R., Milson, B., Wu, X., Wiman, D., Ye, W.J., Young, G., Suhmitted, (Js-Nov-2001) Whithehead Institute/MIT Center for Genome Shimitted (Js-Nov-2001) Whithehead Institute/MIT Center for Genome
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Submitted (07-JUN-2000) Whitehead Institute/MIT Center for Genome
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Center: Whitehead Institute/ MIT Center for Genome Research
                                        Research, 320 Charles Street, Cambridge, MA 02141, USA
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Contact: sequence_submissions@genome.wi.mit.edu
...----- Project_Information
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Center clone name: 79_0_21
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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslawkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
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Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Klein, J., LaRocque, K., Lawazares, R., Macdonald, P., Marquis, N.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Homo sapiens chromosome , clone RP11-79D21, complete sequence.
AC072051
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                  Wiyata, T., Nangaku, M., Inagi, R. and Kurokawa, K. Miyata, T., Nangaku, M., Inagi, R. and Kurokawa, K. Direct Submission
Submitted (15-FEB-2000) Institute of Medical Sciences and Department of Internal Medicine, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa 259-1193, Japan 3 (bases 1 to 4229) Thandler, and Kurokawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-Mar. 2002) Institute of Medical Sciences and Department of Internal Medicine, Tokai University School of Medicine, Bohseidah, Isehara, Kanagawa 259-1193, Japan Sequence update by submitter on Mar 29, 2002 this sequence version replaced gi:18000453.
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Direct Submission
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RESULT 2 AC072051/c

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DEFINITION

LOCUS

ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

JOURNAL REFERENCE AUTHORS

TITLE

AUTHORS TITLE

REFERENCE

promoter

ORIGIN

Matches

source

FEATURES

REMARK COMMENT

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Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, Y., Beda, F., Baldwin, J., Barna, N., Burket, G., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Perreira, P., Fitzhugh, W., Gage, D., Gangon, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gage, D., Grand, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lieu, C., Liu, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehocky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., Mcheeters, R., Medrim, J., Meneus, L., Mihova, T., Minova, T., Minova, T., Minova, T., Minova, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Oliver, J., Peterson, K., Pierre, N., Stange-Thoman, N., Stojanovic, N., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Severy, P., Spencer, B., Vellev, H., Volel, R., Volel, 
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS PHASEL; HTGS_CANCELLED.
HOmo sapiens (human)
Homo sapiens
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Birren, B., Linton, L., Nubbaum, C. and Lander, E.
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                7451. .27484 // rpt family="(CAAAA)n" complement (28183. .28219) // rpt family="MRR" complement (28249. .28325) // rpt family="MRR" complement (29372. .29459) // rpt family="MRR" 29539. .30003
                                                                                                                                                                                                                                                                                                              /rpt family="L2"
31846. .31915
/rpt family="(TGAA)n"
complement(32019. .32103)
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rpt_family="AT_rich"
7451. .27484
                                                                                                                                                                                                              /rpt_family="MER66B"
10596. .30624
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6373. .16374
'note="1328 bp of bacterial transposon insertion in BAC
clone_lib="RPCI-11 Human Male BAC"
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25214. 25358
/rpt_family="L1M4c"
complement(25602. 25854)
/rpt_family="MIR"
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/rpt_family="AT_rich"
14011. 14115
/rpt_family="AT_rich"
/rpt_family="(14942. 15044)
/rpt_family="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excised between these 2 bp"
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25054. .25004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MER3"
/rpt_family="MER3"
/rpt_family="L2"
9276. 941^
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complement(21259. .21386)
/rpt_family="MIR3"
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complement(22788. .22948)
/rpt_family="FRAM"
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/rpt family="L1MC4a"
complement (5742. 5899)
/rpt family="MERSB"
6499. 6816
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834. .4338
                                                    1040. 1077
/rpt_family="AT_rich"
1411. 1747
/rpt_family="LIP"
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3115..3138
/rpt_family="AT_rich"
complement(34877..3828)
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rpt_family="(TAAAA)n"
8332. .19566
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20043. . 20064
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9567. .19587
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9588. .20042
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1659. .1003
'rpt_family="MLT1J"
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5874, .18310
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                          /rpt_family="(T)n"
1040. .1077
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5592. .15773
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233<u>5</u>.
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COOK, A., Cooke, P., DeArellano, K., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gorde, S., Goyette, M., Gage, D., Grand-Pierre, N., Hages, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Linds, G., MacLean, C., Macdonald, P., Marthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Risback, M., Riley, R., Schaub, S., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Trayellio, J., Vassillev, H., Vial, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Submitted, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Submitter, A., and Zody, M., Submitter, A., Submitter, Submitter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 1, 2002 this sequence version replaced gi:11990731. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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/clone_lib="RPC1-11 Human Male BAC"
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/db_xref="taxon:9606"
/chromosome="18"
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STS 31-MAY-2003
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Made, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Tander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers
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                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BV074238 11-MAY-S212P60172FG8.T0 CZECHII/Ei Mus musculus STS genomic, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                Olek, A., Piepenbrock, C. and Berlin, K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1988 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                              88.7%; Score 20.4; DB 6; Length 6182; 95.5%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                               1. .6182
/organism="synthetic construct"
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0; Mismatches
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/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
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Location/Qualifiers
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AX346917.1 GI:18494803
                                                                   synthetic construct artificial sequences.
                                             synthetic construct
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Query Match

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Continuation [5 of 7] of AL928982 from base 400001 (AL928982 Homo sapiens chromosome X c
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The orientation of the sequence is from SP6 to T7 of the PAC clone.
Location/Qualifiers
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2 (bases 1 to 114390)
Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
Submitted (18-APR-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplanies; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114390 bp DNA linear PLN 12-SEP-200
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
PAC clone:P0685G12, complete sequence.
AP005113
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/mol type="genomic DNA"
/cultivar="Nipponbare"
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Pred. No. 3.7e+02;
0; Mismatches 1; Indels 0;
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                                                           80.0%; Score 18.4; DB 9; Length 57941; 95.0%; Pred. No. 3.9e+02; ive 0; Mismatches 1; Indels 0;
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/chromosome="2"
/clone="P0685G12"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of batterial clone contigs of human chrimmosome X, constructed by the Sanger Centre Chromosome X Mapping chromosome X, constructed by the Sanger Centre Chromosome X Mapping
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Human DNA sequence from clone RP4-732K23 on chromosome X, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo. 1 (Dases 1 to 57941) Whitehead, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-JUL-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, Calo 1.SA, UK. B-mail enquiries: thunquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 29, 2003 this sequence version replaced gi:32169142.
                                                                                                                                                                        Gaps
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0
                                                                                                                 Length 687;
                                                                                                                                                                     Indels
                                                                                                         ch 80.0%; Score 18.4; DB 11; Similarity 95.0%; Pred. No. 5.9e+02; 19; Conservative 0; Mismatches 1;
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Center: Wellcome Trust Sanger Institute
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="CZECHII/Ei"<1. .>687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
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/clone_lib="RPCI-4"
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FEATURES

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note="THE1B repeat: matches 295. .364 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw:,
                            ·.
                                                                                                                                                                                                                                                     PRI 10-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CEB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clone-request@sanger.ac.uk
On Feb 11, 1998 this sequence version replaced gi:2808693.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr20
RPS-997K18 is from the library RPCI-5 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LIMC/D repeat: matches 5186. .5568 of consensus"
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/note="LTR16C repeat: matches 93, .364 of consensus"
                            Gaps
                                                                                                                                                                                                                                               HS997K18 110820 bp DNA linear PRI 10-MP Human DNA sequence from clone RP5-997K18 on chromosome 20p12. Contains STSs and GSSs, complete sequence.
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/note="MIR repeat: matches 15. .245 of consensus"
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Location/Qualifiers
                          Indels
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95.0%; Pred. No. 3.7e+02; ive 0; Mismatches 1;
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db_xref="RZPD:RPCIP704K18997"
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                                                                       2 AATGAACTACATAACAACCA 21
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                       Conservative
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HS997K18/c
                                                                                                                                                                                                                                                                       DEFINITION
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                     Matches
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KEYWORDS
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'note="THE1A-internal repeat: matches 1. .371 of consensus"
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/note="BUR1 repeat: matches 12932. .13007 of consensus"
18805. .19024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="12 copies 3 mer tat 86% conserved"
27228. .29379
/note="L1PA15 repeat: matches 3948. .6153 of consensus"
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/note="73 copies 2 mer aa 59% conserved"
74853. .2631
//note="LIMD2 repeat: matches 4815. .6326 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12880. .12789
/note="LTR16C repeat: matches 177. .382 of consensus"
13911. .14962
/note="MER3 repeat: matches 1. .209 of consensus"
14844. .14968
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/note="LiMD repeat: matches 32. .167 of consensus"
23059. .23928
/note="LiMD repeat: matches 974. .1891 of consensus"
24300. .24608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26636. .26978
/note="MLTLAL repeat: matches 14. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7301. .17700
'note="MLTIH repeat: matches 136. .544 of consensus"
                                                                                   /note="THE1A-internal repeat: matches 371. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         b/zs. ...osz.
hote="L2 repeat: matches 2647. .2748 of consensus"
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21636. .22204
/note="L2 repeat: matches 2122. .2710 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 17. .189 of consensus"
11197. .11368
/note="MER5B repeat: matches 13. .172 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="12 repeat: matches 1767. .1940 of consengus"
16528. .16721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER63A repeat: matches 1. .206 of consensus"
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                                                                                                                                                                                                                                                           9921. .10262

// note="THB1B repeat: matches 1. .364 of consensus"
complement(10771. .10852)
// note="match: GSS: Em:AQ187931"
10771. .10825
                                                                                                                                                                       'note="AluSp repeat: matches 1. .311 of consensus"
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24609. .24655
7960, .8026
/note="THELA repeat: matches 1. .41 of consensus"
8027. .9238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 93. .230 of consensus" 5462. .15997
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                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ316710"
10876. .11057
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                                                                                                                                            .9549
                                                                                                                 consensus"
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AC073703 207166 bp DNA linear HTG 18-JUL-2000 Mus musculus clone RP23-16E5, WORKING DRAFT SEQUENCE, 22 ordered

Direct Submission Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:8810320.

2 (bases 1 to 207166) DOE Joint Genome Institute.

REFERENCE AUTHORS TITLE JOURNAL

Sequencing of Mouse Unpublished

REFERENCE AUTHORS TITLE JOURNAL

Web site: http://www.jgi.doe.gov

Center Code: JGI

-----Genome Center Center: Joint Genome Institute

COMMENT

Center Project Name: 1743117 Center clone name: RPCI-23\_16E5

Summary Statistics

Project Information

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 207166)

DOB Joint Genome Institute.

AC073703.2 GI:9256762 HTG; HTGS PHASE2; HTGS DRAFT. Mus musculus (house mouse) Mus musculus

ORGANISM

SOURCE

ртесев

ACCESSION

VERSION KEYWORDS

LOCUS

RESULT 10 AC073703

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Anote="L1PA7 repeat: matches 5807. ,6145 of consensus" 34716. 34947
mote="L1ME repeat: matches 5576. ,5810 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /38576. .38734
/note="L1MA9 repeat: matches 5855. .5989 of consensus"
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/note="LiMA9 repeat: matches 6163. .6270 of consensus"
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/note="LiMD3 repeat: matches 7272, .7330 of consensus"
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15383. .45737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MA2 repeat: matches 6175. .6308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="L1MC4 repeat: matches 7710. .7970 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="L1PA5 repeat: matches 4407. .6141 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 5. .230 of consensus"
50009. .50539
note="LiM4 repeat: matches 3878. .4424 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1P3 repeat: matches 5501. .5554 of consensus"
13334. .43362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="34 copies 2 mer at 67% conserved"
361B1. :36570
/note="LTR16B repeat: matches 38. .458 of consensus"
36610. :36986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MLTIJ repeat: matches 112. .140 of consensus"
14826. .45020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MLT1A1 repeat: matches 37. .233 of consensus"
45035. .45382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L2 repeat: matches 1596. .2008 of consensus"
37799, .37860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MLT11 repeat: matches 74. .135 of consensus"
note="AluSx repeat: matches 39. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="THEIC repeat: matches 1. .371 of consensus"
                       31226, .31518 /
/note="AluJo repeat: matches 1. .299 of consensus"
32108. .32413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="AluSx repeat: matches 1. .300 of consensus"
                                                                                      'note="AluSx repeat: matches 1. .306 of consensus"
                                                                                                                                     .213 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 18.4; DB 9; Length 119420; 95.0%; Pred. No. 3.7e+02; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               35064. .35135 /
/note="18 copies 4 mer tata 68% conserved"
35065. .35132
                                                                                                                                                                                                                                                                                                                   'note="10 copies 3 mer tta 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="22 copies 4 mer acag 72% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="12 copies 2 mer ac 90% conserved"
19354. .49574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52619. .52658
/note="20 copies 2 mer ca 90% conserved"
52970. .53161
                                                                                                              32743. .32894
/note="MIR repeat: matches 50.
                                                                                                                                                                                                34293, .34333
/note="match: STS: Em:G09780"
complement (34293, .34333)
                                                                                                                                                                                                                                                                  note="match: STS: Em:G09898"
4303. .34332
                                                                                                                                                                                'note="match: GSS: Em:B91428"
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                                                                                                                                                          33424. .33614
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Best Local Similarity 95.04
Matches 19; Conservative
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Consensus quality: 193525 bases at least Q40
Consensus quality: 202548 bases at least Q30
Consensus quality: 204188 bases at least Q30
Consensus guality: 10420 bases; agarcse-fp estimation
Quality coverage: 8.2 in Q20 bases; agarcse-fp estimation.
**NOTE: This is a 'working draft' sequence. It currently
consists of 22 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
** 1444 13587; contig of 4743 bp in length
** 13588 13687; gap of unknown length
** 13588 13687; gap of unknown length
** 13588 26532; contig of 12845 bp in length
** 26533 26632; gap of unknown length
** 13588 13687; gap of unknown length
** 13588 13687; gap of unknown length
** 1480 93370; contig of 10282 bp in length
** 1480 93370; contig of 10282 bp in length
** 1480 93370; contig of 10282 bp in length
** 1480 93370; contig of 10282 bp in length
** 1480 93370; contig of 6081 bp in length
** 1480 93370; contig of 6081 bp in length
** 1480 93370; contig of 6081 bp in length
** 99551 gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 11799 bp in length
gap of unknown length
contig of 6552 bp in length
gap of unknown length
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135192:
135292:
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128641
135193
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0; Gaps

7849 AATGAACTACAGAACAACCA 7830

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Birren, 320 (Laries Street, Cambridge, MA 02141, USA)

Birren, 320 (Laries Street, Cambridge, MA 02141, USA)

Birren, 320 (Laries Street, Cambridge), Allen, N.,

Baderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., FittGerald, M., Gage, D., Galagan, J., Gardyna, S.,

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Hall, J., Morton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Maddrim, J., Mencus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

Nguyen, C., Nicol, R., Morbu, C., O'Connor, T., O'Donnell, P.,

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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Talamas, J., Tesfaye, S., Theodore, J., Troylam, K., Travers, M.,

Vassiltev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (23-ApR-2003) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141 USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker:html

H. Happer, A. & Green, P. (1996-1997)
Submitted (30-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contag of 100 bp
contig of 1316 bp in length
contig of 100 bp
contig of 1083 bp in length
gap of 100 bp
contig of 1312 bp in length
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contig of 1107 bp in length
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contig of 2372 bp in length
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contig of 1151 bp in length
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contig of 1546 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L26973
Center clone name: 378 B 3
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6356:
6456:
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8951:
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10302:
11848:
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5041
6357
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9052
10203
111849
111949
113056
113156
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17410
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     JOURNAL
                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC132190 31678 bp DNA linear HTG 23-APR-2003 Mus musculus clone RP23-378B3, WORKING DRAFT SEQUENCE, 41 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.4; DB 2; Length 207166;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels 0;
contig of 2606 bp in length
contig of 5410 bp in length
gap of unknown length
gap of unknown length
contig of 2372 bp in length
contig of 1575 bp in length
gap of unknown length
contig of 15175 bp in length
contig of 1868 bp in length
contig of 1868 bp in length
gap of unknown length
contig of 1898 bp in length
gap of unknown length
contig of 1998 bp in length
gap of unknown length
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95.0%;
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Zembek, L., Zimmer,
Direct Submission
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Best Local Similarity
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79651: contig of 5280 bp in length
80061: gap of 100 bp
85312: contig of 5851 bp in length
86012: gap of 100 bp
96395: contig of 10383 bp in length
96495: gap of 100 bp
142116: contig of 45821 bp in length
142416: gap of 100 bp
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201149: contig of 5873 bp in length
263498: gap of 100 bp
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263498: gap of 100 bp
316678: contig of 53180 bp in length
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/note="agmembly_fragment"
3563. .4940
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Unpublished

2 (bases 1 to 124786)

Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.

Direct Submission

Submitted (16-MAR-2002) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 124786)

Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,

Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
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Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 124786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 1 clone RP4-580019, complete sequence. AC115285 AL359872 AC115285.2 GI:21629400
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0%; Score 18.4; DB 2; Length 316678; Best Local Similarity 95.0%; Pred. No. 3.4e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0;
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Sequencing vector: plasmid; L08752; 59% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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Contact: uwgchtgs@u.washington.edu
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Center clone name: RP4-580019 (sc0808)
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Homo sapiens
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Direct Submission
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240 230 220 25-cont	6-bp overlap -bp overlap	h sequence quality	ssembly program. en reduced to quality zero.				ows unless otherwise noted: anded or sequenced with an	high quality data (i.e., Phred e to resolve all sequencing	repeats; all regions were belone or more than one M13	firmed by restriction digest.	by Multiple Complete Digest	experimentally derived digest fragments is given below	nce consists of both insert and	cutoff (approximately 400-800 bp)	icant remaining discrepancies icted values. Uniquely ordered		Carbine CocherMan	oedre i map		449		2814										. 0
Phrap; version 0.990319 : 124541 bases at least Q40 : 124757 bases at least Q30 : 124780 bases at least Q20 86; sum-of-contigs 6.2x in Q20 bases; sum-of-cont	s: MJ38837, 17366-bp overlap J355178, 46965-bp overlap	ssment: annotated with sequence quality	bases have been reduced to quality zero.			.1 file.	nished as follows unless otherwise noted: her double-stranded or sequenced with an	or covered by high quality data (i.e., Phred tempt was made to resolve all sequencing	npressions and repeats; all regions were one plasmid subclone or more than one M13	sembly was confirmed by restriction digest.	en validated by Multiple Complete Digest	noe-predicted fragments is given below	digested sequence consists of both insert and accurately represent the entire circular Bac	www a variable cutoff (approximately 400-800 bp)	are no eignificant remaining discrepancies untal and predicted values. Uniquely ordered		-Man Franchist Coalbarden	rightime Sequermap	3464	5558 449	512	2814	1247	4695	3373	4630	1454	9110	1751	5564	546	4849
10319 sast Q40 sast Q30 sast Q20 sum-of-cont	Overlapping Sequences: 5': RP1-149P10 AL138837, 17366-bp overlap 3': RP5-947L8 AL355178, 46965-bp overlap	Sequence Quality Assessment: This entry has been annotated with sequence quality			are not generally visible t are available as part	entry's ASN.1 file.	e was finished as follows unless otherwise noted: were either double stranded or sequenced with an	alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing	<pre>problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13</pre>	d the assembly was confirmed by restriction digest.	Sequence Validation: This sequence has been validated by Multiple Complete Digest	fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.	The electronically-digested sequence consists of both biggs.  Vector, in order to accurately represent the entire direct and	ents below a variable cutoff (approximately 400-800 bp)	in the table. There are no eignificant remaining discrepancies between the experimental and predicted values. Uniquely ordered		-Man Franchist Coalbarden	ordvermap rigitatiic ordvermap	13702 14292 3464	5671 5558 449	4326 512	9842 2814	3110 1247	2659 4695		1984 4630	3602 1454	2449 9110	<800 1751	<800 5564	5 757 546	2 3853 4849

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The manufalta include a primates catarinin; Hominidae; Homo.

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Homo sapiens 12 PAC RP1-157K6 (Roswell Park Cancer Institute Human
PAC Library) complete sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                / Match 79.1%; Score 18.2; DB 9; Length 124786; Local Similarity 87.0%; Pred. No. 4.5e+02; Lonservative 0; Mismatches 3; Indels 0;
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/note="Single subclone region"
124398. .124468
/note="Single subclone region"
124783. .124786
                                                                                                                                                                                                                                          'note="Single subclone region"
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       .42459
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SOURCE

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Submitted (29-AUG-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 157653)
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 157653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-5EP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 157653) (college Section 127653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 29, 1998 this sequence version replaced gi:3327895. INFORMATION: http://www.ngsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 157653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-NOV-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 157653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-07N-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Flaza, Houston, TX 77030, USA
                                                                                                              Direct Submission
Submitted (20-UUN-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Weinstock, G. and Gibbs, R.
                                                                   2 (bases 1 to 157653)
Worley, K.C.
                                                                                                                                                                               (bases 1 to 157653)
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the BST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

us-09-889-611a-19.rge

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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                    at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                                                  QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of bases quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                complement(1. .2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MLT1E2-internal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MLT1E2-internal"
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18920. .19201
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'function="clone overlap"
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                                                                                                                                                                                                                                                                                                                'organism="Homo sapiens"
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complement(1961, .2045)
/rpt_family="L2"
3408_ .3501
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[6143. .16381
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4784. .5062
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14787. 14807
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.7707. .17926
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7688. .8058
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                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP1-157K6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="AluY"
4225. .4754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MIR" 3872. 4164
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/standard_name
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Dipublished

Birren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bodyladiter, B., Brown, A., Burkett, G., Bagolavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Poyle, W., Ferreira, P., Fitzhugh, W., Gage, D., Gangan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehorzky, J., McCarthy, M., McEwan, P., McGurla, R., McMernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurla, R., McMernan, K., McMeres, J., Mnrphy, T., Naylor, J., Morman, C.H., O'Connor, T., O'Donnor, J., O'Donnor, J., Stange-Thoman, N., Stojanovic, N., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Volel, R., Charles, J., Volel, R., Volel, R., Charles, J., Volel, R., Vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202398 bp DNA linear HTG 08-MAR-2000
Homo sapiens clone RP11-689C19, WORKING DRAFT SEQUENCE, 33
unoxidered pieces.
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Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                             79.1%; Score 18.2; DB 9; Length 157653; 87.0%; Pred. No. 4.4e+02;
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174122 bases at least Q40
Consensus quality: 192877 bases at least Q20
Insert size: 194000; agarose-fp
Insert size: 199198; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
....------ Project Information
                                                                                                                                                                                     3; Indels
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                                        /rpt_family="AT_rich"
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Homo sapiens (human)
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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 3.4 in Q20 bases; sum-of-contigs
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2: gap of 100 bp
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gap of 100 bp

contig of 13055 bp in length

gap of 100 bp

contig of 13463 bp in length

gap of 100 bp
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Query Match 79.1%; Score 18.2; DB 2; Length 202399; Best Local Similarity 87.0%; Pred. No. 4.38+02; Matches 20; Conservative 0; Mismatches 3; Indels 0;
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                                                                         AC020965 238554 bp DNA linear HTG 10-FEB-2000
Mus musculus clone RP21-82116, WORKING DRAFT SEQUENCE, 80 unordered
                                                                                                                                                                                                                                              Direct Submission
Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Secone Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center Geneer Institute
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                 AC020965.1 GI:6691265
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 80 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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2582: contig of 1259 bp in length
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0; Gaps Query Match 79.1%; Score 18.2; DB 2; Length 238554; Best Local Similarity 87.0%; Pred. No. 4.3e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0;

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Search completed: March 24, 2004, 23:01:21 Job time : 515.584 secs

us-09-889-611a-19.rng

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Query Match 100.0%; Score 23; DB 3; Length 23; Best Local Similarity 100.0%; Fred. No. 1.1; Matches 23; Conservative 0; Mismatches 0; Indels
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Aaa71436 Human meg
Aaa71434 Human meg
Ab134015 Human imm
Ab423440 Human cbN
Ab423444 Oligonucl
Ab4232599 DNA encod
Ad47985 Rat gene
Abk31277 Signal tr
Ab170238 Chemicall
Aas61181 Human gen
Ab82180 Prostate
Ad41173 Rat gene
Ab133617 Human imm
Acf6209 Photorhab
Aca13407 Prokaryot
Ab127492 Drosophil
Aai57764 Human dig
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Aai57764 Human dig
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(without alignments)
811.351 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                         3373863 seqs, 2124099041 residues
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AAA71435 standard; DNA; 1431

RESULT 2 PAA71435 Human megsin promoter fragment DNA.

(first entry)

01-DEC-2000

AAA71435;

25-JAN-2000; 2000WO-JP000350.

WO200043528-A1.

27-JUL-2000.

Homo sapiens

99JP-00015667.

25-JAN-1999;

(KURO/) KUROKAWA K. (MIYA/) MIYATA T.

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region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (1); (2) a cell transformed by the
                                                                                                                                                                                                                                                                                                                                             This invention describes a novel DNA sequence (I) representing a promoter
                                                                                                                                                                                                                                                                DNA for promoter region of megsin useful for screening proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30 BP; 13 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       Example 5; Page 40; 45pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA71434 standard; DNA; 128 BP.
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                                                      25-JAN-2000; 2000WO-JP000350
                                                                                           25-JAN-1999; 99JP-00015667
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Best Local Similarity
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                                                                                                                               (KURO/) KUROKAWA K. (MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KURO/) KUROKAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40200043528-A1
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                  27-JUL-2000.
                                                                                                                                                                                          Miyata T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA71434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (especially transcription factors). This sequence represents a fragment of the human megsin promoter which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1431 BP; 466 A; 266 C; 303 G; 394 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                         Promoter; megsin; human; protein isolation; screening. ss.
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Disclosure; Fig 2; 45pp; Japanese

WPI; 2000-543257/49.

diyata T;

1 GAATGAACTACATAACAACCACC 23

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Query Match
Best Local Similarity 100.0
Matches 23, Conservative

AAA71448 standard; DNA; 30 BP

RESULT 3

01-DEC-2000 (first entry)

AAA71448;

WO200043528-A1

Homo sapiens.

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Gaps

2 AATGAACTACATAACAACCACC 23

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above vector, and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors). This sequence represents the human megsin promoter which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, ansemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                    95.7%; Score 22; DB 3; Length 128; 100.0%; Pred. No. 3.3; tive 0; Mismatches 0; Indels
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                                                                                                    Sequence 128 BP; 44 A; 29 C; 24 G; 29 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 1988.
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                                                                                                                                                                                                                      2 AATGAACTACATAACAACCACC 23
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                               22; Conservative
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Human; foetal tissue antigen; 88; antiinflammatory; neuroprotective; immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; breast neoplasm; carebroascular disorder; cardiac arrest; cerebrovascular disorder; cerebrai ischaemla; anglogenesis; nervous system disorder; wound healing; epithelial cell proliferation; food additive.
                                                                                                                                            Human cDNA encoding a novel foetal antigen, SEQ ID No 734.
                    1310 AATAAACTACATAACAACCACC 1289
                                                                            AAS34210 standard; cDNA; 350 BP
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2000US-0225214P.
2000US-0225266P.
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2000US-0225758P.
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01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
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2000US-0224519P.
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2000US-0226681P.
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2000US-0227182P.
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24-FEB-2000; 2000US-0184664P.
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                                                                                                                      17-DEC-2001 (first entry)
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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11-JUL-2000;
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18-AUG-2000;
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2000US-0230439P.
2000US-0231243P.
2000US-0231244P.
2000US-02314413P.
2000US-0231414P.
2000US-0232080P.
2000US-023239P.
2000US-023239P.
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2000US-023239P.
2000US-023239P.
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2000US-0234223P.
2000US-0234274P.
2000US-0234997P.
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2000US-0236370P.
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2000US-0246610P.
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2000US-0246524P.
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17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
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2000US-0246474P.
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17-NOV-2000;
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08-NOV-2000;
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PR 17-NOV-2000 2000US-024921P.

PR 17-NOV-2000 2000US-024924P.

PR 17-NOV-2000 2000US-024926P.

PR 17-NOV-2000 2000US-024929P.

PR 17-NOV-2000 2000US-024929P.

PR 17-NOV-2000 2000US-024929P.

PR 17-NOV-2000 2000US-024930P.

PR 17-NOV-2000 2000US-025199P.

PR 17-NOV-2000 2000US-025199P.

PR 17-NOV-2000 2000US-025199P.

PR 05-DEC-2000 2000US-025199P.
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Query Match 74.8%; Score 17.2; DB 5; Length 350; Best Local Similarity 86.4%; Pred. No. 4.64-02; Matches 19; Conservative 0; Mismatches 3; Indels COY 2 AMTGRACTRACRACCACC 23

145 AATGAACTCCATTACAATCACC 124

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Gaps

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RESULT 7 ABQ23445

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                            Human; cytosine methylation, 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                        Oligonucleotide for detecting cytosine methylation SEQ ID NO 10036.
                                                                                                                                                                                                                                                                                                                                    Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                         Guetig D;
                                                                                                                                                                                                                                                         Berlin K,
ABQ23445 standard; DNA; 580 BP
                                                                                                                                                                                     01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                                                                         01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                 05-SEP-2000; 2000DE-01044543
                                       (first entry)
                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                           WPI; 2002-371829/40.
                                                                                                                                             WO200218632-A2
                                                                                                                           Homo sapiens.
                                       12-JUL-2002
                                                                                                                                                                  07-MAR-2002
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated c, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptidenucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nearous, and of a wide range of succeiving and respirators systems etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Abgl3410-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  llustrate the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ54121 represent genomic DNA sequences used to illustrate the meth
for determining the degree of cytosine methylation described in the
disclosure of the invention
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      74.8%; Score 17.2; DB 6; Length 580; 86.4%; Pred. No. 4.8e+02;
                                     Indela
                                   0; Mismatches
Query Match
Best Local Similarity 86.4<sup>§</sup>
Matches 19; Conservative
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## 254 AATCAACTACATATCAACCGCC 275 2 AATGAACTACATAACAACCACC 23

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AAS72599 standard; cDNA; 1350 BP.

AAS72599/c

13-FEB-2002 (first entry)

田政紀城市政

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ABQ23444 standard; DNA; 580 BP
                                                           ABQ23444;
                 ABQ23444/c
RESULT 8
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methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert or cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of follygoucheotides and/or peptide-mucieic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABO13410-2002 ABO54121 represent genomic DNA sequences used to illustrate the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining the degree of
                                                                                                          Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for determining the degree of cytosine methylation described in the disclosure of the invention
                                                               Oligonucleotide for detecting cytosine methylation SEQ ID NO 10035.
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74.8%; Score 17.2; DB 6; Length 50
Best Local Similarity 86.4%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AATCAACTACATATCAACCGCC 306
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                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.
                  12-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                            Homo sapiens.
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reaction (PCR) primers, to laterate polymerate polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polymeptide and polymuleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to isolated polynucleotide (I) and polypeptide (II)
                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.8%; Score 17.2; DB 5; Length 1350; 86.4%; Pred. No. 5.1e+02;
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DNA encoding novel human diagnostic protein #8403.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 8403; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD47985 standard; DNA; 4789 BP.
                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
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les 19; Conserv
                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                                                                                                        WO200175067-A2.
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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucvel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kut increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an animal of one or more of the cativity in an enthod for identifying a compound useful in treating activity in an enthod for identifying a compound or small molecule that regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound or small molecule that regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the regulates the cativity in an enthod for identifying a compound the cativity in an enthod for ident
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (cCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the specification) which encodes one of the polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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Rat; ds; gene; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                                                       L4-AUG-2002; 2002WO-US025765.
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                                                                                                               Rattus norvegicus
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                                                                                                                                                                        WO2003016475-A2
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated the bases of a segment of chemically pretreated DNA of genes associated invention may be described as cytostatic. The object of the invention is convide the chemically modified DNA of genes associated with cell signalling, as well as oligonuclectides and/or PNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequences of the for this patent is not represented in the printed py the specification, but is based on sequence information supplied by the
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                                                       Cell signalling; cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
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Chemically treated cell signalling DNA sequence complementary to#64.
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                                                                                                                                                                                                                                                                                                       29-JUN-2001; 2001WO-EP007471.
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                                                                              tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                         WO200202807-A2.
                                                                                                                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA, e.g. cellines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                            Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                     Signal transduction associated gene modified complementary DNA #60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 120; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000DE-01032529.
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                                                    23-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           WO200200926-A2.
                                                                                                                                                                                                                                                                             Homo sapiens.
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Matches

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WPI; 2002-471335/50.
P-PSDB; ABG61913.
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                                                                                       13-OCT-2000;
               18-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 224 nucleic acid sequences comprising at least selected from 43 known genes for complementary sequences. The chemical pretreated gene associated with gene regulation selected from 43 known genes for complementary sequences. The Chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR stromm, Saether-Chotzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer-associated DNA sequence #116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 140; 26pp; English
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                                                                                                                                                                                                                                                                                              Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK92230 standard; DNA; 12879 BP
                                                                                                                                                               2000DE-01019058.
2000DE-01019173.
                                                                                                                                                                                                30-JUN-2000; 2000DE-01032529.
                                                                                                                          06-APR-2001; 2001WO-EP003968
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Matches 19; Conservative
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                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
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                                                    WO200177375-A2.
                   Homo sapiens.
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07-APR-2000;
                                                                                       18-OCT-2001
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The present invention relates to methods of detecting a prostate cancer-
associated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with prostate cancer-
associated polymuclectides (designated PC genes) that selectively
hybridise to a sequence that is at least 80% identical to them. The
prostate cancer-associated polymuclectide sequences are differentially
prostate cancer-associated polymuclectide sequences are differentially
cypressed in prostate tumour tissue or in prostate cancer and are useful for
(e.g. mice, sheep and dogs). The methods of the invention are useful for
diagnosing and treating prostate cancer in mammals. The prostate cancer-
associated genes are useful for diagnosing or treating prostate cancer,
as well as for identifying modulators of prostate cancer or agents that
inhibit prostate cancer. The nucleic acid sequences are particularly
useful in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 394-397; 436pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EOSB-) ROS BIOTECHNOLOGY INC
                                                                                                                             08-DEC-2000; 2000US-00733288.

08-DEC-2000; 2000US-00733742.

24-UAN-2001; 2001US-025957P.

16-WAR-2001; 2001US-0276888P.
                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-2001; 2001US-0286214P
30-APR-2001; 2001US-00847046
04-MAY-2001; 2001US-0288589P.
12-OCT-2001; 2001WO-US032045
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Query Match

74.8%; Score 17.2; DB 4; Length 13202;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indel8 0;

12091 AATGAACTCCATTACAATCACC 12070

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Search completed: March 24, 2004, 22:28:19 Job time : 124.427 secs

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CC162058 ii81b04.b
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GenCore version 5.1.6
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000000000000000000000000000000000000000		cc162058 ii81b04.b1 vilab04.b1 vilab04.b1 vilab04.b1 vilab04.gec cc162058.ccc162058.cccc dea mays Eukaryota; vilabonicolor clade; panitolor color contact: w. co
		es have bed
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/organism="Zea mays"
/mol_type="genomic DNA"
/etrain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Other GSSs: PUJGG81TB
Contact: Cathy Whitelaw
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Fax: 301-838-0208
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/clone lib= WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between O.8 and 3 kb and were cloned into the vector (.x/y
reads in Milample). .b/g reads in pUCl9). The same ligation
was transformed into DH5a."
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Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ400233 684 bp DNA linear GSS 03-OCT-200 1M0166L21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0166L21 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0166 Tow: L column: 21
Seg primer: CGTTGTPAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                              /mol_type="genomic_DNA"
cultivar="B73"
/do_xref="taxon:4577"
/clone="ii81b04"
/lab_host="DH5a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
              Class:
Class: Shotgun
High quality sequence stop: 569.
Location/Qualifiers
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/clone="UUGC1M0166L21"
                                                                                                                organism="Zea mays"
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Seq primer: -21M13UnivFwd
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.05 inch orifice at constent velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were adaptored to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of pNDG2 (gil 4732114|gb|AFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The absared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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(bases 1 to 782)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
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/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
//note="Weetcr: PWA2Avv; Purified genomic DNA from M.
musculus G57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone_lib="NCI_CGAP_Mam6"
Other GSSs: NDL.60D18.T7
Contact: Brendan Loftus
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NDL.60D18.SP6 Notre Dame Liverpool Aedes aegypti genomic clone
NDL.60D18, genomic survey sequence.
                                                                                                                                                                 CC090422 785 bp DNA linear GSS 16-APR-2003 CSU-K331.9P3.T7 CSU-K33r Aedes aegypti genomic clone CSU-K33r.9P3,
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Fax: 301-838-0208
Bmail: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado State University.
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
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/note="Vector: pBeloBAC11; Site_1: HindIII"
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     Indels
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Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC en equencing of Aedes aegypti
Unpublished (2003)
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     1;
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                                                                                                                                                                                                                                                                       Aedes aegypti (yellow fever mosquito)
                                                                                                                                                                                                                                                                                                                                                           Joseph 1 (Dases 1 to 785)
Loftus, B., Shetty, J., Severson, D., Br
End sequencing of Aedes aegypti BACs
Unpublished (2003)
Other_GSSs: CSU-K33r.9P3.SP6
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .785
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Rexville"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan Loftus
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7159"
/clone="CSU-K33r.9P3"
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                                                                       500 regacracaracaaccacc 481
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                                     4 TGAACTACATAACAACCACC 23
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CC090422
CC090422.1 GI:29947659
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   19; Conservative
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AUTHORS
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
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CC134385
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/clone="NDL.60D18"
/clone lib="Notre Dame Liverpool"
/clone lib="Notre Dame Liverpool"
/clone lib="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DES/2261 601330149F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3707436 5', mRNA sequence.
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.b column: 13
High quality sequence stop: 340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 18.4; DB 28; Length 927; 95.0%; Pred. No. 2.6e+03; Live 0; Mismatches 1; Indels 0
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/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5_months"
/lab_host="DH108"
                                                       9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                              Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                          /organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
Department of Eukaryotic Genomics IIGR
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/clone="IMAGE:3707436"
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:7159"
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/strain="FVB/N"
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Verjovaki-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweller, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukar, G.C., Soares, M.B., Gargioni, C., Kawano, T., Sedrigues, V., Madeira, A.M., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C., and Dias-Neco, E.
                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="non-glandular-haired subtracted cDNA library" /note="glandular-haired versus non-glandular-haired reciprocal cDNA subtraction with CLONTECH PCR-Select cDNA
                                                                                                                                                                                                                                                      Expressed sequence tags subtracted in reciprocal fashion between glandular-haired and non-glandular-haired full sibs of alfalfa Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD183415 307 bp mRNA linear BST 14-SEP-
MS1-0038U-A246-G09-U.B MS1-0038 Schistosoma mansoni cDNA clone
MS1-0038U-A246-G09.B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 307)
                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, GMPRC, PSERU; Department of Agronomy
                                                                                                                                                                                                                                                                                                                                                                                                       Kansas State University
Throcokmorton Hall, Manhattan, XS 66506, USA
Tel: 785 532 7116
Fax: 785 532 6167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 79.1%; Score 18.2; DB 10; Best Local Similarity 87.0%; Pred. No. 3.2e+03; Matches 20; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3879"
/tissue_type="Leaf and stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Riley X KS224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dhays@genes.alfalfa.ksu.edu
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CD183415.1 GI:34713619
  AW698814.1 GI:7581400

    (bases 1 to 129)
    Hays, D. and Skinner, D.

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Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                          Contact: Hays DB
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                                                     Medicago sativa
Medicago sativa
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CD183415/c
                                                     SOURCE
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/clone lib="Homo sapiens PlaceNTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL572872
AL572872 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI034YH01 3-PRIME, mRNA sequence.
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall; Ste 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequescope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2214.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO34CDOINPl&cluster=2214.r. Contact
cgi-bin/cluster.cgi?seq=CSODIO34CDOINPl&cluster=2214.r. Contact
Feng Liang Email: filangn@lifetech.com/RL:
http://fulllength.invitrogen.com/InvitroGen.Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO34CDOINPI.
Location/Qualifiers
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                 Length 999;
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                                                                                                                                                                                                                 1; Indels
                                                                                                                                                           80.0%; Score 18.4; DB 10; 95.0%; Pred. No. 2.6e+03;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CS0DI034YH01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAATGAACTACATAACAACCAC 22
                                                                                                                                                                                                                                                                                                                             464 TGAACCACATAACAACCACC 483
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                                                                                                                                                                                                                    Conservative
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Best Local Similarity
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FEATURES

RESULT 8

ORIGIN

VERSION KEYWORDS

COMMENT

RESULT 7

DRIGIN

EST 14-SEP-2003

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Gaps

Length 129; Indels ô

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CD188719/c
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1 (Dases I to 309)

1 (Dases III)

1 (Dases III)

2 (Dulson, P. L. T. O., Ohlweiler, P. P., Reis, E. M., Ribeiro, M. A., Sar, R., Madeira, M. B. M., Wilson, R. A., Madeira, M. B. M., Wilson, R. A., Madeira, A. M. B. M., Wilson, R. A., Menck, C. F. M., Setubal, J. C., Leite, L. C. and Dias-Neto, E.

Transcriptome analysis of the accelomate human parasite Schistosoma
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                                   Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MS1-0038U-A246 row: 9 column: G.
Location/Qualifiers
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This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.ig.usp.br/schisto/
Plate: MG1-0024U-A317 row: 10 column: H.
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Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
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0; Mismatches 3
                                                                                                                                                                                                                                                            /organism="Schistosoma mansoni"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pGEM T-easy"
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                    Tel: +55-11-3091-2173
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Fax: +55-11-3091-2186
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Best Local Similarity
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KEYWORDS
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/organism="Schistosoma mansoni"

Bource

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Strigerious manazon; Platyhelminthes; Trematoda; Digenea; Strigeridida; Schistosomatoidea; Demarco, R. Martins, E.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Parias, L.P., Bonaldo, M.F., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
                                                                                                                                                                                                                                                                                                                                                                                       CD188719 313 bp mRNA linear EST 14-SEP-2003 MS1-0063U-A262-A04-U.B MS1-0063 Schistosoma mansoni cDNA clone MS1-0063U-A262-A04.B, mRNA sequence.
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This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MSI-0063U-A262 row: 4 column: A.
Location/Qualifiers
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Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                             Gaps
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79.1%; Score 18.2; DB 14; Length 309; 87.0%; Pred. No. 3.1e+03; tive 0; Mismatches 3; Indels 0
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                                                                                                                                           1 GAATGAACTACATAACAACCACC 23
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                                 Best Local Similarity 87.0 Matches 20; Conservative
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Best Local Similarity
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Matches

ACCESSION

VERSION KEYWORDS

SOURCE

REFERENCE AUTHORS

RESULT 12 CD165299 LOCUS

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Schietosoma manson:

Sukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

El (Dases I to 531)

Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E. B.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,

Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,

Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,

Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,

Nascimento,A.L.T.O., Ohlweller,F.P., Reis,E.M., Ribeiro,M.A.,

Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,

Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.

Transcriptome analysis of the accelomate human parasite Schistosoma
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Strigeidida, Schistosomatoidea, Schistosomatidae, Schistosoma.
1 (Bases I to S37)
Verjovski-Almeida, S., DeMarco, R., Martins, E. A. L., Guimaraes, D. E. M., Ojopi, E. P. B., Paquola, A. C. M., Piazza, J. P., Nishiyama, M. Y. Jr., Ritailima, T. P., Adamson, R. B., Pabton, P. D., Bonaldo, M. F., Coulson, P. S., Dillon, G. P., Farias, L. P., Gregorio, S. P., Ho, P. L., Leite, R. A., Malaquias, L. C. C., Marques, R. C. P., Miyasato, P. A.,
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Bmall: vericed quep.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MS1-0063U-A351 row: 11 column: H.
Location/Qualifiers
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MA3-9999U-V243-H11-U.B MA3-0001 Schistosoma mansoni cDNA clone MA3-9999U-V243-H11.B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Diversidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo -
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/lab_host="in vitro culture"
/clone_lib="MS1-0063"
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CD189864.1 GI:34719847
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1 (bases I to 317)

1 (bases I to 17)

2 (bases I to 17)

2 (bases I to 17)

3 (bopi.z. P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, J.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C., and Dias-Neto, E.
Transcriptome analysis of the acoelomate human parasite Schistosoma
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                                                                                                                                                                                                                                                                    CD165299 317 bp mRNA linear EST 14-SEP-2003
ML1-0095T-D144-B05-U.G ML1-0095 Schistosoma mansoni cDNA clone
ML1-0095T-D144-B05.G, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/Plate: ML1-0095F-D144 row: 5 column: B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Ouimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
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      Indels
      3;
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/organism="Schistosoma mansoni"
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/db_xref="teaxon:6183"
/clone="ML1-0095T-D144-B05.G"
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   0; Mismatches
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/clone_lib="ML1-0095"
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                                                              1 GAATGAACTACATAACAACCACC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
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1 (bases I to 556)

1 (bases I to 556)

1 (bases I to 556)

2 (bases I to 556)

3 (boyl, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
                           Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
Rodrigues,V., Madelra,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
Setubal,J.G., Leite,L.C.C. and Dias-Neto,E.
Transcriptome analysis of the accelomate human parasite Schistosoma
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This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
amnotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MA3-9999U-V243 row: 11 column: H.
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Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                              Contact: Dr. Sergio Verjovski-Almeida
Departamento de Biognimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
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Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
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22879926
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Fax: +55-11-3091-2186
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Fax: +55-11.3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MA3-0001U-L241 row: 7 column: H.
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/db_xref="taxxon:6183"
/clone="MA3-0001U-L241-H07.B"
/sex="mixed pool"
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/clone_lib="MA3-0001"
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March 24, 2004, 21:53:36; Search time 552.809 Seconds (without alignments) 1960.127 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                   3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                              1 aaccaccttagtcagatactacttt 25
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Maximum Match 100%
Listing first 45 summaries
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25
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AF234618 Homo sapi AC072051 Homo sapi	Homo	Rattus	AL590440 Human DNA AC009946 Homo sapi		4 14	Mus	AC129307 Mus muscu	AC122243 Mus muscu	уэг мив 9 Наетој	AC101370 Mus muscu	AC135510 Mus muscu	AC0108442 Homo sapi	במ	AL929371 Mouse DNA	AC110204 Mus muscu	00 0	מסמ	00 0	ACIU3411 KACLUS NO AX656609 Sequence	BC054091 Mus muscu	M33960 Mouse plasm	M24067 Rattus norv	AX409680 Sequence	JO5206 Rat plasmin	X94912 H.sapiens P	ACI13157 Homo sapi	AP002543 Arabidops	98880	5044			linear PR	region and partial sequence.			a, Vertebrata, Buteleostomi; ini, Hominidae, Homo.	and Kurokawa,K. mesangium-predominant gene, megsin	
SUMMARIES : ID	AF234618 AC072051						0		0		AC101370	AC135510						2 AC121487				10 MUSPAI1 6 ax827499	0	AX409680	0	HSPR22	AC11315	AP0025	ACOO	AC02504	ALIGNMENTS		4229 bp	ne, promoter	8130	•	Chordata; Craniata; V Primates; Catarrhini;	Inagi,R.	
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Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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Center clone name: 79_D_21
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/clone="RP11-79D21"
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Homo sapiens chromosome , clone RP11-79D21, complete sequence.
AC072051
                                                                                                                                                     Submitted (29-MAR-2002) Institute of Medical Sciences and Department of Internal Medicine, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa 259-1193, Japan Sequence update by submitter on Mar 29, 2002 this sequence version replaced gi:18000453.
                                               Submitted (15-FEB-2000) Institute of Medical Sciences and Department of Internal Medicine, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa 259-1193, Japan 3 (bases 1 to 4229)
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93.6%; Score 23.4; DB 9; Length 4229;
Best Local Similarity 96.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                       Miyata,T., Nangaku,M., Inagi,R. and Kurokawa,K. Direct Submission
2 (bases 1 to 4229)
Miyata,T., Nangaku,M., Inagi,R. and Kurokawa,K.
Direct Submission
                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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/product="megain"
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3 (Bases 1 to 157284)

Shiren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Boqualavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, A., Cook, R., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farzelan, E., Britzhugh, M., Gagago, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Ilaev, I., Johnson, R., Jones C., Kamat, A., Karlas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., McEwan, P., McHor, T., Merphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Donne
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Submitted (07-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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rpt_family="(CA)n"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Barsien, V., Beda, F., Bordwingalter, B., Brown, A., Burkett, G., Callynore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Grach, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Illev, I., Johnson, K., Jones, C., Kanni, L., Karni, J., Klein, J., Lakocque, K., Lamacres, R., Landers, T., Lehoczky, J., Klein, J., Lakocque, R., Lawazres, R., Landers, T., Lehoczky, J., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPhoczky, J., McCarthy, M., McEwan, P., McGurk, A., McGarnan, K., McPhoczky, J., McCarthy, M., McEwan, P., McGurk, A., McGarnan, K., McPhoczky, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollywar, T.M., Ollver, J., Peterson, K., Pierre, N., Santos, R., Schauer, S., Severy, P., Spencer, B., Theodore, J., Tirrell, A., Traesran, Trainino, J., Vashin, N., Stojanovic, N., Subramanian, A., Talamas, J., Vashin, V., A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Vonnell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Direct Submission Bubmitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 189092)

3 (bases 1 to 189092)

4 Donkill, Boukhgalter, B., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Ragenien, J., Campoplano, A., Camarata, J., Campoplano, A., Camarata, J., Camgoplano, A., Camarata, J., Camgoplano, A., Camarata, J., Camgoplano, A., Camarata, J., Campoplano, A., Canarata, J., Camarata, 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC027524 189092 bp DNA linear HTG 27-MAR-2
Homo sapiens chromosome 18 clone RP11-317G1 map 18, 3 unordered
pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.6%; Score 23.4; DB 9; Length 157284; 96.0%; Pred. No. 1.1; 11 indels 0; Mismatches 1; Indels 0;
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AC027524.4 GI:21307437
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens (human)
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 18, clone RP11-317G1
                                              /rpt family="(CAAAA)n"
complement(28183..28219)
/rpt family="MIR"
complement(28249..28325)
/rpt family="MIR"
complement(29372..29459)
/rpt family="MIR"
29539..30003
/rpt_family="MIR"
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31846. .31915
/rpt_family="(TGAA)n"
complement(32019. .32103)
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30596. 30624
/rpt_family="AT_rich"
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family="AT_rich" . .27484
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family="L2"
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Best Local Similarity 96.0%;
...hes 24; Conservative
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AX346917.1 GI:18494803

KEYWORDS

VERSION

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Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeAzellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., DeAzellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gardyna, S., Ginde, S., Govette, M., Graham, L., Gardyna, S., Ginde, S., Govette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karteas, A., Kells, C., LaRocque, K., Linds, C., Maclean, C., Macdonald, P., Major, J., Marquis, N., Maclean, C., Macdonald, P., Major, J., Marquis, N., Maclan, C., Macdan, C., Morchy, P., Marquis, N., Marquis, N., Milova, T., Milova, T., Milova, T., Milova, V., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Olliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Raback, M., Riley, R., Schauer, S., Schupback, R., Saman, J., Rosetti, M., Roy, A., Santos, R., Stanger Thomann, Stojanovic, N., Strauss, N., Subzamanian, A., Talanas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Tayin, D., Vell, R., Voll, R., Wilson, B., Wu, T., Wyman, D., Ye, W., Direct, Submission, J., Zimmer, A. and Zody, M., Direct, Submission, J., Linds, J., Janes, J., Teefaye, S., Vanna, G., Submission, J., Zimmer, A. and Zody, M., Janes, J., Janes, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUL 1, 2002 this sequence version replaced gi:11990731. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
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85759: gap of 100 bp
161014: contig of 77255 bp in length
161114: gap of 100 bp
189092: contig of 25978 bp in length.
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/clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
/chromosome="18"
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Allen,C., Allen,H., Algbrooks,S., Amin,A., Anguiano,D., Allen,H., Algbrooks,S., Amin,A., Anguiano,D., Allen,H., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Brawlo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Carder,A., Cavazos,I., Casazi,H., Center,A., Cardens,V., Carter,K., Cavazos,I., Chen,G., Chen,Z., Chen,Z., Chen,G., Chen,Y., Chen,Z., Chen,G., Chen,Y., Chen,Z., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davils,M.L., Davils,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Dinh,H., Divya,K., Draper,H., Duyan-Rocha,S., Dunn,A., Durbin,K., Dinh,H., Divya,K., Braner,C., Bann,Rocha,S., Dunn,A., Durbin,K., Dinh,H., Garza,M., Garser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,M., Guevara,W., Gunaratne,P., Haaland,M., Falggy,N., Forbes,L., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Hogson,A., Hogues,M., Harnandez,B., Hanes,A., Henderson,N., Hernandez,J., Jackson,A., Hollins,B., Howells,S., Hladun,S.L., Hodgson,A., Hognes,M., Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Liu,J., Liu,W., Liu,Y., Lousacce,S., Lopez,J., Lorensuhewa,I., Loulseged,H., Lorado,R.J., Lu,X., Mandin,P., Martin,R. Marrina,R. Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus clone CH230-121G8, WORKING DRAFT SEQUENCE, 5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="unassigned DNA"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                   Olek, A., Plepenbrock, C. and Berlin, K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1988 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.8%; Score 20.2; DB 6; Length 6182;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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/organism="synthetic construct"
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Location/Qualifiers
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synthetic construct
synthetic construct
artificial sequences.
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                                                                                                                                                      AUTHORS
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PAT 01-FEB-2002

linear

DNA

Sequence 1988 from Patent WO0200928, AX346917

RESULT 4 AX346917/c

DEFINITION ACCESSION

LOCUS

66579 AACCACCTTAGTCAGATACTATTTT 66603

1 AACCACCTTAGTCAGATACTACTTT 25

us-09-889-611a-20.rge

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Direct Submission

List Userials Sugaranteed Content of Medicine Content Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23665344.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entiraly of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzco, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sheety, J., Shvartsbeyn, A., Sieter, C.D., Smals, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soas, J., Sreimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waddron, L., Walker, B., Wang, J., Warren, S., Warren, R., Wel, X., White, F., Willson, R., Wilson, R., Willson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, S., Wallson, R., Wilson, S., Wang, J., Zhao, J., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Poll, R.A., Smith, H.O., Neins, C., Land, C., Land, R., Smith, D.R., Smith, R., Smith
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NOTE: This is a "working draft' sequence It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
Submission
Submitted (19-FBB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 346601)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113609: contig of 113609 bp in length
113709: gap of unknown length
166592: contig of 52883 bp in length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgge-help@bcm.tmc.edu
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Unpublished
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REFERENCE

REFERENCE AUTHORS

COMMENT

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Direct Submission

Submitted (05-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeates; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP: WORNUEP; Information on the WORNPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALS90440 63011 bp DNA linear PRI 05-APR-2001
Human DNA sequence from clone RPI1-12C17 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 63011)

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13 166692: gap of unknown length 3 343924: contrig of 177232 pp in length 25 344024: gap of unknown length 25 345211: contig of 1187 bp in length 25 345211: gap of unknown length 25 345601: contig of 1290 bp in length. Location/Qualifiers
                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:BH263748"
complement(176165..177055)
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                                  /clone="CH230-121G8"
36757. .38228
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="clone boundary
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AL590440/c
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IMPORTANT: This sequence is not the entire insert of clone RP11-12C17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP11-12C17 is at 63011 in this sequence. The true left end of clone GS1-11815 is at 33117 in this sequence. The true right end of clone RP11-67L3 is at 100 in this
RP11-12C17 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="TIGGER1 repeat: matches 863. .1014 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR24 repeat: matches 250. .480 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER44C repeat: matches 81. .359 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312. .598
/note="HERV23 repeat: matches 1. .274 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 2617. .2735 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2069. .2441 of consensus"
045. .3405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744. .5847
note="L2 repeat: matches 2513. .2722 of consensus"
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12003. .12029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2441. .2513 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="THE1C repeat: matches 1. .243 of consensus"
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note="MIR repeat: matches 121. .182 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157. .8456
hote="AluSx repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSp repeat: matches 1. .312 of consensus"
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note="MIR repeat: matches 40. .182 of consensus"
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note="MIR repeat: matches 16. .121 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match: GSS: Em: AQ530043"
                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                   clone="RP11-12C17"
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'note="MER41-internal repeat: matches 1. .86 of consensus"
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18354. 18753
18754. ...18829
18754. ...18829
Indee="LTRNA-Lys-AAG repeat: matches 1. .76 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  note="L1M4 repeat: matches 3865. .4250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L8830. ,18860
/note="LTR10C repeat: matches 580. .609 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18861. .18926
/note="MER51-internal repeat: matches 1186. .1250 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MluSg1 repeat: matches 1. .309 of consensus" 20891. .21410
/note="WER51-internal repeat: matches 2802. .3327 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18928. .19335
/note="WEK51-internal repeat: matches 1181. .1593 of
                                                                                                                note="MER41A repeat: matches 1. .554 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MBR51-internal repeat: matches 1593, .2802 of
                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2255. .2518 of consensus"
15846. .16227
                                                                                                                                                                                                                                                                                                                                                                                                                                   16446. .16803
hote="MER51A repeat: matches 1. .371 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                        16251. .16440 -
/note="WER20 repeat: matches 1. .179 of consensus"
                                                                               .205 of consensus"
                       .2030. .12761
/note="LTR8 repeat: matches 1. .691 of consensus"
repeat: matches 79. .102 of consensus"
                                                                                                                                                                                                                                                                         16804. .18061
/note="WER51-internal repeat: matches 1. .1250 of
                                                                                                                                                                                                                                           note="MIR repeat: matches 3. .259 of consensus" 4622. .14743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="10 copies 4 mer atat 85% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="22 copies 2 mer at 75% conserved"
                                                                                                                                                                                   complement (14302. .14756)
/note="match: STS: Em:HSPE03H12"
                                                        12762. .12848
'note="MIR repeat: matches 102.
12903. .13455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ254526"
complement(18141. .18319)
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/note="match: GSS: Em:AZ707492"
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/note="match: GSS: Em:AQ417380"
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8149. .18192
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complement(18181. .18319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (18181.
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consensus"

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AC139347 21-FEB-2003 MA linear HTG 21-FEB-2003 Mus musculus chromosome UNK clone RP24-334F11, WORKING DRAFT SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (31-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 205202)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Feb 1, 2003 this sequence version replaced gi:28173257.
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 205202)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 201546 bases at least Q40 Consensus quality: 202453 bases at least Q30 consensus quality: 20288 bases at least Q30 consensus quality: 20288 bases at least Q20 lnsert size: 229000; agarose-fp lnsert size: 229000; agarose-fp Quality coverage: 17.08 in Q20 bases; sum-of-contigs Quality coverage: 11.09 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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gap of unknown length

contrig of 4492 bp in length

gap of unknown length

contrig of 5482 bp in length

contrig of 10133 bp in length

gap of unknown length

gap of unknown length
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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Unpublished
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McPherson, J.D. and Waterston, R.H.
                                      137651 ACCACCTTAGTCACATGCTACTT 137629
2 ACCACCTTAGTCAGATACTACTT
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Submitted (19-DBC-1999) Genome Sequencing Center, Washington
Submiversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 169072)
Waterston, R.H.
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Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                                                                                                                       /note="L1M4 repeat: matches 3768. .3836 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                Gaps
        21393, .21893
/note="MBK57-internal repeat: matches 3520. .4039 of
                                                                                                                          21937. .24469
/note="MER51-internal repeat: matches 5199, .7816 of
                                                                                             .1699 of
                                                                                                                                                                                    24471. .24809
/note="WER51A repeat: matches 1. .371 of consensus"
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On Dec 20, 1999 this sequence version replaced gi:5836211.
Center project name: NH0012C17.
Location/Qualifiers
1. .169072
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                  79.2%; Score 19.8; DB 9; Length 63011; 91.3%; Pred. No. 66;
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                                                                 21873. .21983
/note="MER61-internal repeat: matches 1584.
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Homo sapiens clone RP11-12C17, complete sequence.
AC009946
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/db_xref="taxon:9606"
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Waterston, R.H.
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3 (bases 1 to 169072)
Waterston, R.H.
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                                                  consensus,
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Best Local Similarity 91.3%
Matches 21, Conservative
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LOCUS

FEATURES COMMENT

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VIDEQNISESKVALVYGQMNEPPGARMRVGLTALTMAEYFRDVNEQDVLSFIDNIFRF
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|qene="trnR"
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H+-ATP synthase; photosystem I polypeptide I; psaI gene; rbcL gene;
ribulose-bisphosphate carboxylase large subunit; tRNA-Arg; trnR
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Submitted (05-AUG-1997) Sutter A., Johannes Gutenberg-Universitaet
Mainz, Institut fuer Allgemeine Botanik, Muellerweg 6, 55099 Mainz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutter, A., Philipps, A. and Wild, A. Picea ables chloroplast genome fragment of 8,7 kb including atpE, atpB, rbcL, trnR, accD, and psaI unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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38432: contig of 15047 bp in length 38532: gap of unknown length 52633: contig of 14101 bp in length 52733: gap of unknown length 102557: contig of 49824 bp in length 102657: gap of unknown length 153484: contig of 50827 bp in length 153584: gap of unknown length 205202: contig of 51618 bp in length
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Matches 20; Conservative
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Direct Submission
Submitted (13-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 121227)
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Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 11, 2000 this sequence version replaced gi:6042116.
                                                                                                      TLDVIAFFESENEPAHSDPLHSEDESYKDHITFCQIETGITDAIQTGIGQINGLFIALG
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SALYIPQKDNRLLYVSILTSPTTGGVTASFGMLGDIIJAEPKAXIAFAGKIVIDQTLG
QKVIRDFQVTFBILFGRGLFDLIVPRNILMCYLLSELFYVLQSSS"
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5 (bases 1 to 121227)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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The sequence of Homo sapiens BAC clone RP11-531P14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="Photosystem I polypeptide I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19.2; DB 8;
Pred. No. 1.7e+02;
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Sulston, T.B. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
/db_xref="GI:2/04.2/v"
/db_xref="GOA:047039"
/db_xref="SWISS-PROT:047039"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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/gene="psa1"
7765. 7875
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 76.8%;
1 Similarity 87.5%;
21; Conservative
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Best Local Similarity
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCPherson, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Reci-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RP11-531P14 contains a transposon in the growth of the clone, which is not part of the submitted sequence.

Location/Qualifiers
                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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2436_ .2451
/note="similar to EST AA648276 (NID:g2574705) ns20d03.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                    all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the right is RP11-500G18, 200 base pair overlap. Actual start of this clone is at base position 1 of RP11-531P14; actual end is at base position 34258 of RP11-500G18.
                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saptens@wateson.wustl.edu
                                                                                                                                                                                                                                                                                                                                 between neighboring data submissions.
                                                                                                                                                 Center project name: H NH0531P14
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6965_.7417
/rpt_family="Retroviral"
8545_.8614
/rpt_family="MIR"
                                                                                                                       ----- Summary Statistics
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NEIGHBORING SEQUENCE INFORMATION:
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/db_xref="taxon:9606"
/chromosome="2"
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/rpt_family="L2"
4249. .4270
/rpt_family="AT_rich"
5090. .5111
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1805. .2244
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Direct Submission
Submitted (11-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 14, 2003 this sequence version replaced gi:29244816.
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Mus musculus BAC clone RP23-328L1 from chromosome 18, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milbul, M.
Sequencing of Mus musculus
Unpublished (2001)
3 (bases 1 to 191085)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 191085)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (26-MAR-2003) Genome Sequencing Center, 4444 Forest Park
Submitted (26-MAR-2003) Genome Sequencing Center, 4444 Forest Park
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 191085)
Isak,A. and Bielicki,L.
                                                                                                                                                                                                                                                                                                                  Gaps
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Unpublished (2001)
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Contact: submissions@watson.wustl.edu
----- Summary Statistics
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                                                              /rpt_family="L1"
30967. .31089
/rpt_family="L1"
31097. .31555
                                                                                                                             /rpt_family="L1"
31555. 31840
/rpt_family="L1"
33392. 33438
/rpt_family="L2"
33730. 33784
rpt_family="Alu"
10439. .30706
                               rpt family="Alu"
30722. .30879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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33821. .34119
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Wilson, R.
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7.2pt_family="L2"
86589. .26936
7.0cte="match_to EST Al081859 (NID:g3418651) ov24c04.x1"
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19378. .19486
/rpt_family="Retroviral"
19521. .1999.
20171. .20317
/rpt_family="Retroviral"
20318. .20318
..20618
/rpt_family="Alu"
20611. .20656
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. family="MER1_type"
19. .17073
._family="Alu"
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rpt family="Retroviral"
4387. .15337
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7. .15381
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23608. .23783
/rpt_family="MIR"
55428. .25451
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29097. .29622
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:5484. .25599
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5403. .160>F
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28540, 200-1
          /ipt_family="L2"
9965. .10026
/rpt_family="L2"
10057. .10199
/rpt_family="L2"
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11189. .11353
/rpt_family="L2"
11588. .11793
/rpt_family="L2"
/rpt_family="L2"
11792. .12080
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|12102. .1220
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| 14002. | 114002.
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25974. .26000
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family="L2"
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29645, .30187
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# Center project name: M\_BA0328L01

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:
The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is overlapped by AC114820 and AC121874.

Location/Qualifiers

source

FEATURES

1. .191085 /organism="Mus musculus"

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1033. 1180 /rpt\_family="Alu" 1451. 1655 /rpt\_family="B2" 1908. 1990 7908. .1990 /rpt\_family="L1" 2060. .2102 /rpt\_family="B4" 2073. .2211 repeat\_region repeat\_region repeat region repeat\_region repeat\_region

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island (%GC=72.3, o/e=0.94, #CpGB=114)" /rpt\_family="B4" 15985. 16138 /rpt\_family="B4" family="B4" .15949 'rpt\_fa 1585<u>1</u>.

> repeat\_region repeat\_region

repeat\_region

repeat\_region repeat\_region repeat\_region repeat\_region

Matches

RESULT 12 AL807818/c

DEFINITION

LOCUS

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

ö

Gaps

; 0

3; Indels

Length 194425;

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AC129307 198602 bp DNA linear HTG 25-AUG-2002
Mus musculus chromosome UNK clone RP24-200K10, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1 to 198602)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (28-JUL-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19862)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkway, St. Louis, MO 63108, USA.
On Aug 25, 2002 this sequence version replaced gi:22138611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence, It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 195486 bases at least Q40
Consensus quality: 195486 bases at least Q20
Insert size: 202000; agarose-fp
Insert size: 197629; sum-of-contigs
Quality coverage: 12.83 in Q20 bases; sum-of-contigs
Quality coverage: 11.64 in Q20 bases; sum-of-contigs
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Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- Genome Center -----
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                              Score 19.2; DB 5;
Pred. No. 1.1e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                            165858 AAACACTTTAGTCAGATACTAGTT 165835
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McPherson, J.D. and Waterston, R.H.
                                /clone="CH211-225H24"
/clone_lib="CHORI-211"
   /db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                               1 AACCACCTTAGTCAGATACTACTT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                       ch 76.8%;
1 Similarity 87.5%;
21; Conservative
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                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AC129307/c
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ORGANISM
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AUTHORS
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AUTHORS
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KEYWORDS
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This sequence was finished as follows unless otherwise noted: all regions were either double-etranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

BEN: SMISSPROT; Tr:, TREMBL; Wp:, WORMFEP; Information on the WORMFEP database can be found at the WORMFEP database can be found at beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' further information see http://www/Projects/D rerio/fishmask.shtml
CH211225424 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL807818 194425 bp DNA linear VRT 18-FEB-2003 Zebrafish DNA sequence from clone CH211-225H24, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-FEB-2003) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 1.SA, UK. B-mail enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@snger.ac.uk Clone requests: clonerequest@snger.ac.uk On Feb 18, 2003 this sequence version replaced gi:28273001.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      76.8%; Score 19.2; DB 10; Length 191085; 87.5%; Pred. No. 1.1e+02; rative 0; Mismatches 3; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12117 AAACAGCTTACTCAGATACTACTT 12140
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16472. .16523
/rpt_family="Alu"
16697. .16776
                                                                                                                                                                                                                                                                                                                                                                                                                          1 AACCACCTTAGTCAGATACTACTT
                                                                                                                                              /rpt_family="Alu"
16779. .16923
                                                                                                                                                                                                              /rpt_family="B4"
16977. .17064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL807818.14 GI:28412565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
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6218.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Beasley,H.

REFERENCE AUTHORS JOURNAL

COMMENT

1099: contig of 1099 bp in length

be preserved.

/mol\_type="genomic DNA"

source

FEATURES

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AC122243 204584 bp DNA linear ROD 04-NOV-2003
Mus musculus chromosome 17 clone RP23-148C10, complete sequence.
AC122243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherson, J. D. and Waterston, R.H.
McPherson, J.D. and Waterston, R.H.
Direct Submission

Bubmitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 204584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson, R. K.
Direct Submission
Direct (16-58-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 204584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Nov 4, 2003 this sequence version replaced gi:34495085.
                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 204584)
Wilson,R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC100052
AC100052.6 G1:39752800
HTG; HTGS_PHASR1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Genome Center
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143956 AACCAACAAGTCAGATACTACTT 143933
                                                                                              78202 AAACACATTAGTCAGATACTAATT 78179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AACCACCTTAGTCAGATACTACTT 24
                                                                 24
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                                                                 1 AACCACCTTAGTCAGATACTACTT
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                           AC122243.3 GI:38154054
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AC100052/c
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                                                                                                                                                                                                                            7134: contig of 1174 bp in length 7294: gap of unknown length 8773: gap of unknown length 8773: gap of unknown length 14281: contig of 1379 bp in length 14281: contig of 5508 bp in length 14281: gap of unknown length 26301: contig of 11920 bp in length 26401: gap of unknown length 34064: gap of unknown length 47001: contig of 763 bp in length 47001: gap of unknown length 47001: gap of unknown length 65387: contig of 12836 bp in length 65387: contig of 12836 bp in length 65387: contig of 12147 bp in length 129492: contig of 21147 bp in length 129592: gap of unknown length 129592: gap of unknown length 129592: gap of unknown length 139561: gap of unknown length 139561: gap of unknown length 199561: gap of unknown length 199561: gap of unknown length 199602: contig of 641 bp in length 19602: contig of 641 bp in length
2248: contig of unknown length
348: gap of unknown length
711: contig of 1363 bp in length
11: gap of unknown length
70: contig of 2109 br
71: gap of unknown length
70: contig of 2109 br
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26402. .34064
/note="assembly_name:Contig54"
34165. .47001
/note="assembly_name:Contig55
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note≈"aввеmbly_name:Contig51"
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'db_xref="taxon:10090"
'chromosome="UNK"
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Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B. Wusbaum, C. Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., Dartellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Grand-Plerre, N., Hafez, N., Hagopian, D., Hagopian, S., Grand-Plerre, N., Hafez, N., Hagopian, D., Hagopian, S., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Liu, K., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meneus, D., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Oliver, J., Peterson, K., Phunkhang, P., Platre, M., Rawmand, P., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schubback, R., Sewery, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Trayers, M., Wassiliev, H., Venkatamann, V.S., Viel, R., Volan, A., Namanan, D., Young, G., Zainoun, J., Zammer, A. and Zody, M. Direct Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 12, 2003 this sequence version replaced gi:38454416. All repeats were identified using RepeatMasker:
                       Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                            1 (bases 1 to 255457)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 8, clone RP23-32L24
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels 0;
                                                                                                     101651: contig of 101651 bp in length
101751: gap of 100 bp
1128979: contig of 11128 bp in length
112979; gap of 100 bp
204131: contig of 91152 bp in length
234231: gap of 100 bp
233161: contig of 28930 bp in length
233261: gap of 100 bp
                                                                                                                                                                                                                                                                                                                          contig of 7035 bp in length gap of 100 bp contig of 15061 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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us-09-889-611a-20.rng

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

Run on:

March 24, 2004, 18:56:32; Search time 130.899 Seconds (without alignments) 811.351 Million cell updates/sec

US-09-889-611A-20 25 Title: Perfect score:

Sequence:

1 aaccaccttagtcagatactacttt 25

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 29Jan04:\* Database

geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

# SUMMARIES

Description	Aaa71453 Human med	Human,	Aaa71435 Human med	_	Abl34015 Human imm	Continuation (17 o	Aak80155 Human imm	Aak80158 Human imm	Aak80159 Human imm	Aac39949 Arabidops	Ada73153 Rice gene	Acf79501 Mouse pla	Acf79502 Mouse pla	Abt41815 Toxicity	Acf79503 Rat plasm	Abn95829 Gene #232	Abq76613 C. albica	Add46508 Human gen	Aac28947 Human sec	Abl68782 Kidney ca	Aai94790 Human neu	Aah01963 Candida i	Aah01569 Candida d
ΩĪ		AAA71434	AAA71435	AAA71449	ABL34015	AAT42063 16	AAK80155	AAK80158	AAK80159	AAC39949	ADA73153	ACF79501	ACF79502	ABT41815	ACF79503	ABN95829	ABQ76613	ADD46508	AAC28947	ABL68782	AA194790	AAH01963	AAH01569
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% Query Match	100.0	100.0	100.0	88.0	80.8	75.2	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	71.2	70.4	70.4	70.4	70.4	70.4
Score	25	25	25	22	20.2	18.8	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	17.8	17.6	17.6	17.6	17.6	17.6
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Gaps

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Query Match
100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 25; Conservative 0; Mismatches 0; Indels

Sequence 25 BP; 8 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

invention

This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (especially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the

C 24 17.6 70.4 1637 4 AAK69081 25 17.6 70.4 1721 2 AA714565 26 17.6 70.4 1721 2 AA734366 27 17.6 70.4 1721 2 AA732237 29 17.6 70.4 1721 2 AA732237 29 17.6 70.4 2435 6 AB568447 2435 6 AB568447 270.4 4708 1 AAN50415 C 32 17.6 70.4 4708 1 AAN50415 C 32 17.6 70.4 6071 9 AD55299 34 17.4 69.6 2967 4 AA56729 35 17.2 68.8 5149 2 AA732454 37 17.2 68.8 5149 2 AA732454 37 17.6 69.0 694 7 ACF66728 C 40 17 68.0 694 7 ACF66728 C 41 17 68.0 777 7 ABZ42202 C 42 17 68.0 1435 9 AD552966 C 44 17 68.0 1435 9 AD552966 C 45 17 68.0 2516 2 AAV52331	Aak69081 Human imm Aaq14626 Human Gli Aat34366 Plasmid p Aaz32237 Human Gli Aaa88172 pJC99 hum Aba68477 DNA encod		Aas56729 Human BRC Aat32455 Calpain 1 Aat32454 Calpain 1 Acf70412 Photorhab Acf66756 Photorhab Acf66728 Photorhab	Abx06371 S. pneumo Abz42202 Streptoco Adb58387 Toxicity- Adb52966 Primary r Aav52381 Streptoco Aaf29742 Castor be
24 17.6 70.4 25 17.6 70.4 28 17.6 70.4 28 17.6 70.4 31 17.6 70.4 31 17.6 70.4 33 17.6 70.4 35 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.6 69.0 40 17.6 69.0 41 17.6 68.0 42 17.6 68.0 44 17.6 68.0 45.0 47.0 47.0 47.0 47.0 47.0 47.0 47.0 47	AAK69081 AAQ14626 AAT34366 AAZ32237 AAA88172 ABS68447	AAK69082 AAN50415 ADB58365 ADB52939	AASS6729 AAT32455 AAT32454 ACE70412 ACE66756 ACF66728	ABX06371 ABZ42202 ADB58387 ADB52966 AAV52381 AAF29742
24 17.6 70.4 25 17.6 70.4 28 17.6 70.4 28 17.6 70.4 31 17.6 70.4 31 17.6 70.4 33 17.6 70.4 35 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.2 68.8 33 17.6 69.0 40 17.6 69.0 41 17.6 68.0 42 17.6 68.0 44 17.6 68.0 45.0 47.0 47.0 47.0 47.0 47.0 47.0 47.0 47	400000	4100	40055	rr00014
24 17.6 228 17.6 28 17.6 28 17.6 30 17.6 31 17.6 31 17.6 31 17.6 31 17.2 32 17.2 34 17.2 40 17.4 41 17.4 42 17.4 44 17.4 44 17.4 45 17	1637 1721 1721 1721 1721 1721	2790 4708 6071 6071	2967 5149 30967 480 694 697	762 777 1435 1435 2516 3191
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## ALIGNMENTS

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Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
                                                                                                                                                                                                                                   DNA for promoter region of megsin useful for screening proteins.
                                                              Human megsin promoter PCR primer SEQ ID NO: 20.
                                                                                                                                                                                                                                                   Example 4; Page 42; 45pp; Japanese.
              AAA71453 standard; DNA; 25 BP.
                                                                                                                                                            99JP-00015667.
                                                                                                                                              25-JAN-2000; 2000WO-JP000350.
                                            01-DEC-2000 (first entry)
                                                                                                                                                                                                                   WPI; 2000-543257/49.
                                                                                                                                                                           (KURO/) KUROKAWA K.
(MIYA/) MIYATA T.
                                                                                                             WO200043528-A1.
                                                                                             Homo sapiens.
                                                                                                                                                           25-JAN-1999;
                                                                                                                              27-JUL-2000.
                                                                                                                                                                                                   Miyata T;
                              AAA71453;
RESULT 1
        AAA71453
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us-09-889-611a-20.rng

AAA71434

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This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (especially transcription factors). This sequence represents a fragment of the human megsin promoter which is described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 3; Length 1431; 100.0%; Pred. No. 0.095; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1431 BP; 466 A; 266 C; 303 G; 394 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human megsin promoter PCR primer SEQ ID NO: 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 45pp; Japanese
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                                                                                        25-JAN-2000; 2000WO-JP000350.
                                                                                                                                                       99JP-00015667.
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                                                                                                                                                                                                                  (KURO/) KUROKAWA K. (MIYA/) MIYATA T.
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(MIYA/) MIYATA T.
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                                                                                                                                                    25-JAN-1999;
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                                27-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Promoter; megsin; human; protein isolation; screening. ss.
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                                                                                                                                                                                                                                                   AAA71434 standard; DNA; 128 BP
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Best Local Similarity 100.9
Watches 25, Conservative
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(MIYA/) MIYATA T.
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RESULT 3 AAA71435

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above vector, and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors).
AAA/1434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhematic; antiarthritic; antidiabetic; antipsoriatic; antiartisoriatic; antiinflammatcry; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemically modified gene, useful^{\dagger} for associated with abnormal cytosine
                                                                                                                                                                  Gaps
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                                                                                                                              DB 3; Length 30;
1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1988; 32pp + Sequence Listing; German.
                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 1988.
                                                                                            Sequence 30 BP; 12 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                              88.0%; Score 22; DB 100.0%; Pred. No. 1.5 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of diagnosis and treatment of diseases
                                                                                                                                                                                                                         9 AACCACCTTAGTCAGATACTAC 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000DE-01032529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000DE-01043826.
                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
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                                                          invention
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ch 80.8%; Score 20.2; DB 6; Length 6182; 1 Similarity 88.0%; Pred. No. 19; 22; Conservative 0; Mismatches 3; Indels 0;

Query Match Best Local Similarity Matches 22; Conserv

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ntinuation (17 of 19) of AAT42063 from base 1600001 (Haemophilus influenzae complete g
Sequence split into 19 fragments LOCUS AAT42063 Accession Aat42063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34967.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                              Length 110000;
                                                                                                                                                                                                                                                                                                 2; Indels
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Pred. No. 1.2e+02;
0; Mismatches 2;
          1295 AACCACCTTAATCAAATACTATTT 1271
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1 AACCACCTTAGTCAGATACTACTTT 25
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2000US-0205515P.
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2000US-0216647P.
2000US-0216880P.
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2000US-0190076P.
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2000US-0214886P.
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1700001
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1200001
1300001
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                                                                                                                                                                                                                                                                                                 20; Conservative
                                                            Continuation (17 of 19)
                                                                                                                                                                                                                                                                                       Local Similarity
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AAT42063_04
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17-MAR-2000; 2
18-APR-2000; 2
19-MAY-2000; 2
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2000US-0224518P.
2000US-0224519P.
2000US-0225213P.
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2000US-022526F.
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12-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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17-NOV-2000; 2000US-024921BP.
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17-NOV-200
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08-DEC-2000; 2000US-0251866P.

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08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251999P.
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2000US-0251030P.
2000US-0251988P.
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Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 34967; 3071pp + Sequence Listing; English.

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

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23-AUG-2000; 2000US-0229281P.
01-SEP-2000; 2000US-0229281P.
01-SEP-2000; 2000US-0229281P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229344P.
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06-SEP-2000; 2000US-0229344P.
06-SEP-2000; 2000US-0229344P.
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2000US-0246524P.

2000US-0246524P.

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2000US-0246525P.

2000US-0246526P.
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2000US-0246532P
2000US-0246609P
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protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-darived cells. AAK64703 to AAK67694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34970.
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                                                                                                                                                    DB 4; Length 471;
                                                                                                               Sequence 471 BP; 157 A; 69 C; 118 G; 127 T; 0 U; 0 Other;
                                                                                                                                                                                  4; Indels
                                                                                                                                                 74.4%; Score 18.6; Di
84.0%; Pred. No. 78;
ative 0; Mismatches
                                                                                                                                                                                                                                   AAGGACCTTGGGCAGATACTACTTT 407
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2000US-018664P.
2000US-0186464P.
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2000US-0199123P.
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2000US-0199123P.
2000US-0199123P.
2000US-0205467P.
2000US-021513F.
2000US-0215486F.
2000US-0215486P.
2000US-0215487P.
2000US-0215487P.
2000US-0215487P.
2000US-0215487P.
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2000US-0225213P.
2000US-0225213P.
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22-AUG-2000; 2000US-02271B2P.
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                                                                                                                                                              Local Similarity 84.0
nes 21; Conservative
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
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14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
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Matches
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RESULT 9
AAK80159
ID AAK80159 standard; DNA; 471 BP.
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14-SEP-2000; 2000US-0232398P

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34971.
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72-AUG-2000; 2000US-022668IP-
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16-MAR-2000; 2000US-0189874P
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14-AUG-2000;
14-AUG-2000;
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                                                           AAK80159;
                                          AAXE4951 to AAXE4702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient, s genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
complyancieotides may be used to produce the secreted (I), by inserting the
mucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polymucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAX64703
cc diagnose and treat immune/haematopoietic-derived cells. AAX64703
cc diagnose and treat immune/haematopoietic-derived cells. AAX64703
cc AAX87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAX64912 to AAX64950 and AAM82169
cc represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 471 BP; 157 A; 69 C; 118 G; 127 T; 0 U; 0 Other;
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                                                                                                                         2000US-0249215P.
2000US-0249216P.
2000US-0249217P.
2000US-0249218P.
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2000US-0249245P.
2000US-0249264P.
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2000US-0250160P.
2000US-0250391P.
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2000US-0249299P.
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2000US-0249212P
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2000US-0251479P
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2000US-0235836P.
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AAX54951 to AAX64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
c activity, and can be used in gene therapy and vaccine production. (I)
c proteins and polynucleotides may be used in the prevention, diagnosis and
c treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
ct that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c protein. (I) proteins and polynucleotides may be used to prevent,
c nucleic acids into a host cell and culturing the cell to express the
c protein. (I) proteins and polynucleotides may be used to prevent,
c ancers and cranter memune/haematopoietic-related diseases, especially
c cancers and cancer metastases of haematopoietic-derived cells. AAX64703
c to AAX87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAX54912 to AAX54950 and AAM82169
cc represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 34971; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.4%; Score 18.6; I
84.0%; Pred. No. 78;
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ID AAC39949 Btandard; DNA; 1523 BP.
06-DEC-2000; 2000US-02518/79P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
11-DEC-2000; 2000US-025199P.
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Best Local Similarity
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15-JUL-1999;
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Identifying at least one gene involved in plant resistance or response to
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e Z, Zhu T, Zou
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Whitham S, Xie Z,
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Pred. No. 90;
0; Mismatches
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99US-016076BP.
99US-0160770P.
99US-0160814P.
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99US-0161360P.
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99US-0161992P.
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                99US-0158232P
                         99US-0158369P
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les 21; Conservative
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                                 13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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Katagiri F,
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14-OCT-1999
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26-0CT-1999
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                                                                                           The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 compatises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an unlinfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
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pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating a warm-blooded vertebrate animal having a medical condition, e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or glomerulosclerosis, comprises administering a plasminogen activator
                                                                                                                                                                                                                                                                                                                                                     Gaps
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thrombolytic; antiadethmatic; antiinflammatory; nootropic;
neuroprotective; antidepressant; nephrotropic; vulnerary;
antiseborrhoeic; dermatological; antiarteriosclerotic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                   ô
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                                                                                                                                                                                                                                                                                                                74.4%; Score 18.6; D
84.0%; Pred. No. 93;
ive 0; Mismatches
                                                              Claim 27; SEQ ID NO 6479; 899pp; English.
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/product= "Mouse PAI-1"
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ses 21; Conservative
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(DECL/) DECLERCK P J.
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Matches
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Disclosure; Page 73-76; 91pp; English.

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2002US-0370144P
   inhibitor-1 inhibitor.
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01-NOV-2001;
21-NOV-2001;
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keloids, apocrine cysts, acne, atherosclerosis, ageing,
hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.4%; Score 18.6; DB 9; Length 2999; 84.0%; Pred. No. 98; 1.ve 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2999 BP; 728 A; 810 C; 743 G; 718 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AACCACCTTAGTCAGATACTTT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACF79502 standard; cDNA; 2999 BP
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P-PSDB; ABR63127.
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The present sequence is that of cDNA encoding mouse plasminogen activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce transgenic animals of the invention, useful for screening potential PAI-1 inhibitors can be used to treat a warm-blooded vertebrate animal having a medical condition, e.g. alopecia, undesired weight loss, Alzheimer's disease, systemic amyloidosis, myelofibrosis, atherosclerosis, ageing, male pattern baldness, keloids, apocrine cysts, acne, atherosclerosis, ageing, or a wound (claimed). A method of testing a therosclerosis ageing to a composition to a transgenic animal having a PAI-1 gene incorporated into its genome, and observing an amellorating change in the animal indicative of inhibition of PAI-1 activity, the change being an impal indicative of inhibition of PAI-1 activity, the change being an impal indicative of inhibition of PAI-1 activity, the change being an impal indicative of inhibition and activity, the change being an indicative pulmonary disease, alopecia, undesired weight loss such as anorexia, Alzheimer's disease, systemic amyloid deposition, systemic ampliants, myelofibrosis, glomerulosclerosis, male pattern baldness,
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hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
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Pred, No. 98;
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Disclosure; Page 78-81; 91pp; English.
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19-UUN-2001, 2001US-0298925F.

10-UUL-2001, 2001US-0303807F.

10-UUL-2001, 2001US-0303800F.

20-UUL-2001, 2001US-0303810F.

28-MUG-2001, 2001US-0315047F.

27-SEP-2001, 2001US-0324928F.
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2001US-0331805P.
2001US-0336144P.
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21-FEB-2002; 2002US-0357842P.
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Matches 21; Conservative
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Castle A, Elashoff M;

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The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a cissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polymucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                              Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
                                                                                                                                                                     Johnson K, Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page; 446pp; English.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370247P.
17-APR-2002; 2002US-0372794P.
21-APR-2002; 2002US-0371679P.
                                                                                                                                                                     Porter M,
                                                                                                                     (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                           profile to a database.
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74.4%; Score 18.6; DB 7; Length 3053; 84.0%; Pred. No. 98; tive 0; Mismatches 4; Indels 0; Sequence 3053 BP; 773 A; 806 C; 762 G; 712 T; 0 U; 0 Other; Query Match

2665 AACCACCTTAGTTAGATAATCTTTT 2689 1 AACCACCTTAGTCAGATACTATT 25 à

21; Conservative

Matches

Local Similarity

ACF79503 standard; cDNA; 3053 BP L8-DEC-2003 ACF79503; RESULT 15 

(first entry)

Rat plasminogen activator inhibitor-1 cDNA.

Plasminogen activator inhibitor-1; PAI-1; rat; transgenic; thrombolytic; antiasthmatic; antiinflammatory; nootropic; neuroprotective; antidepressant; nephrotropic; vulnerary; antiseborrhoeic; dermatological; antiarteriosclerotic; hepatotropic; gene; ss.

Rattus sp

/product= "Rat PAI-1" Location/Qualifiers 119. .1327 /\*tag=

WO2003071267-A1

28-AUG-2003

19-FEB-2003; 2003WO-US005008

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The present sequence is that of cDNA encoding rat plasminogen activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce transgenic animals of the invention, useful for screening potential PAI-1 inhibitors as but PAI-1 inhibitors can be used to treat a warm-blooded vertebrate animal having a medical condition, e.g. alopecia, undesired vertebrate animal having a medical condition, e.g. alopecia, undesired to vertebrate animal having a medical condition, e.g. alopecia, undesired to alomerulosclerosis, male pattern baldness, Reloids, apocrine cysts, acne, atherosclerosis, ageing, or a wound (claimed). A method of testing a candidate composition for PAI-1 inhibition arminal having a PAI-1 gene incorporated into its genome, and observing an ameliorating change in the inforative of inhibition of PAI-1 activity, the change being an improvement of a vascular thrombotic disorder, asthma, chronic obstructive pulmonary disease, alopecia, undesired weight loss such as anorexia, Alzheimer's disease, alopecia, undesired weight loss such as anorexia, Alzheimer's disease, systemic amyloid deposition, systemic amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne, atherosclerosis, or a wound (claimed) hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
                                                                                                                                                                                                                              Treating a warm-blooded vertebrate animal having a medical condition, e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or glomerulosclerosis, comprises administering a plasminogen activator inhibitor.
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                                                                                                                                       Eren M;
                      19-FEB-2002; 2002US-0358061P.
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84.08;
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(DECL/) DECLERCK P J.
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2665 AACCACCTTAGTTAGATATCTTTT 2689

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Search completed: March 24, 2004, 22:28:23 Job time : 134.899 secs

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AI349205 ta74b03.x
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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28 AQ586782
9 AI188862
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			18.6	74.4	364	13	BY171910	ш,	2
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	П	н	æ	٠.	411	13	BY688349	щ	3Y688349 BY688349
	-1 -	01.0	œ .	٠.	413	133	BY573260	щ	3Y573260 BY573260
	F	ω 4	, a	4.47	414		BY513444 RV503440	щ	3Y513444 BY513444 3Y503440 BY503440
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	υ O	0	œ ·		441	10	BF282272	ш	3F282272 EST446977
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		er u		4.4.	450	2 5	BBB28056	.u	3B828056 BB828056
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	m r	٥,			532	Ξ.	BU760030	ш,	3U760030 UI-R-FS1-
	יי רי	٦,	m a	74.4	556 565	120	BF556719	<b>24</b> 6	3F556719 UI-R-CO-g
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	m	-			722	14	CB571286	, 0	BS71286 AGENCOURT
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	) J 4	h C	o a	# 4	1126	2 0	A2139264	<b>4</b> C	12139264 SP 01// B
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	ক ক	4+ ru	18.2	72.8	236	0 0	BF552977 AW992361	Мα	BF552977 UI-R-C2-n
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	DEFINITION	ITION	BX7	BX783787 X(	XGC-edd	Silı	8/0 bp Silurana tropica	calis cDNA clone T	ilnear EST 10-DEC-2003 lone TEGG059i02 3', mRNA
			sed	lence.	1		4	1	
	ACCESSION	SION	BX7	BX783787	į				
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	SOURCE		Sill	irana to	ropical		(western clay	awed froa!	
	ORG	ORGANISM	Sill	irana to	tropicalis				
			Euk Ampl	iryota;	Metazoa; Batrachia	)a; (		ı; Craniata; Vertebrata; Mesobatrachia; Pipoides	a; Euteleostomi; lea; Pipidae;
	00000		Хеп	podina	e; Silu	rane			
	AUTHORS	HORS	Cro	(Dases Jing, M.1	D.R., A	o)		or, R.	l. and Rogers, J.
	TIL	TITLE	Sang	Sanger Xenopus tropicalis E Unpublished (2003)	opus tz d (2003	opido.	alis EST proje	ject 2001 (11_2003)	
	COMMENT		Sand	cact: C: ver Inst	roning Litute	MDR			
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			Sanc	LI: troj Ter Xend	pøsange Jous tr	r.ac	ST pr	oiect 2001	
			TRO	ICALIS	SEQUEN		1g0591	02.q1kT7	
			Thie	uencing pr B sequence	primer: T/ nce is from	fron F	Bridor	tion	(XGC) library
			COD	tructe	Š	Aaron M.	f. Zorn.		
_			CDN	was o.	ligo dT	pri	primed from 5ug	of poly A+ RNA	from egg.

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us-09-889-611a-20.rst

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AI349205 244 bp mRNA linear EST 16-FEB-1999 ta74b03.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2049773 3',
                                                                                                                                                                                                                                                                                   AI188862 Soares placenta 8to9weeks_2NbHP8to9W Homo sapiens CDNA clone IMAGE:1724926 3' similar to gb:X15414 ALDOSE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 549).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1099 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                              Score 19.8; DB 28; Length 467; Pred. No. 2.1e+02;
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                                                                                       Indels
                                           ch 79.2%; Score 19.8; Di Similarity 91.3%; Pred. No. 2.1e. 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1724926"
                                                                                                                                                                             428 ccacciraarcacarreraciri 450
                                                                                                                                   3 CCACCTTAGTCAGATACTACTTT 25
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AI188862.1 GI:3740071
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Unpublished (1997)
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AI188862/c
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: T7
Class: BAC ends.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site_2: NotI
Host: Escherichia coIi XLI-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                       /note="Vector: pGS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pGS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPC111 Ruman Male BAC Library"
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Venter,J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                           80.8%; Score 20.2; DB 13; Length 870; 88.0%; Pred. No. 1.7e+02;
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Unpublished (1997)
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                 /organism="Silurana tropicalis"
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/clone="HRSQ059102"
/dev_stage="egg"
/dev_stage="egg"
/lab_host="Escherichia coli XLI-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 ACCAACCTTAGTCAGATACTAATTT 307
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                                                                                                                                                                                                                                                                     clone_lib="XGC-egg"
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trimmed with the aid of the trim_alt option. Vector identified with
                     cross match v0.990329.
Plate: TWW8011 row: M column: 8
Seg primer: GTAATACGACTCACTATAGGG.
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Location/Qualifiers
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/db_xref="GDB:3847724"
                                                                                                             1. .569
/organism="Sus scrofa"
                                                                                                                                                                                                    /tigsue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4PIG"
                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H85044.1 GI:1063699
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                                                                                                                                                                                                                                                                   Email: cgapbe-remail.nih.gov
Tisaue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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I (Bases I to 569)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="NCI_CGAP_HSC2"
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from bone marrow, stem cells 34+38+, cDNA made by oligo-dr priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library,
                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 244)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Thuor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF793467 1inear 569 bp mRNA linear 888857 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LiNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 347 Std Error: 0.00
Seq primer: -400P from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryos representing early developmental stages Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.8%; Score 19.2; DB 9; ilarity 87.5%; Pred. No. 3.1e+02; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="stem cell 34+/38+"
                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2049773"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="DH108"
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AI349205.1 GI:4086411
                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
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Best Local Similarity
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CF793467
LOCUS
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                                                                                                                                  REFERENCE
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ys66b06.81 Soares retina N2b4HR Homo sapiens CDNA clone
IMAGE:219731 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4RR"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stops: 299 Source: INAGE Consortium, LLNL This clone is available robalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
/note="Wector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 319)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                             Length 569;
                                                                                                                                                                             75.2%; Score 18.8; DB 14; Length 90.9%; Pred. No. 6.3e+02; cive 0; Mismatches 2; Indels
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Mus materials (Botheria; Craniata; Vertebrata; Buteleostomi; Makaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases I to 364)

1 (Bases I to 364)

2 (Masses II. Masses, T. Maschi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyosam, J., Mogami, A., Matsuda, H., Batsel, K., Tomaru, Y., Haseqawa, Y., Mogami, A., Cothia, C., Corbani, L.E., Cousines, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garsin, C., Godzik, P., Frazer, K.S., Gaasterland, T., Gustincich, S., Hirokawa, N., Jackson, I.J., Marvis, E.D., Kanagani, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Kawaji, H., Kawasawa, Y., Redzierski, R.M., King, B. L., Konagaya, A., Marthionni, L., Marchionni, L., Mokenius, J., Mixi, H., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Pertea, G., Pesole, G., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Yang, I., 
BY171910 364 bp mRNA linear EST 10-DEC-2002 BY171910 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone I830090319 5', mRNA sequence.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, TBurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 74.4%; Score 18.6; DB 14; Length 319; Best Local Similarity 84.0%; Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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Mus musculus
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PUBMED
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ACCESSION VERSION KEYWORDS SOURCE

RESULT 7 BY171910 REFERENCE

JOURNAL

COMMENT

TITLE

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Email: genome-resegge.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Aizawa,T., Increase,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imcata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Saski,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 377)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Kuchaba,T., Le,M., Lenno,G., Marra,M.,
Parsons,J., Rifkin,L., Rouchba,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Tissues were provided by David A. Hume ( Depts. of Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="1830090J19"
/tissue type="bone marrow"
/cell_type="macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
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Best Local 8
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SET191771 Normalized rat lung, Bento Soares Rattus sp. cDNA clone (MINTS) 63, end, mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                               Email: est@watson.wustl.edu
High quality sequence stops: 370
Source: IMAGE Consortium, LINLI, fortact the
This clone is available royalty-free through LINL, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 590 Std Error: 0.00
Seq primer: Promega -21ml370.
High quality sequence stop: 370.
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                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="retina"
/dev stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3847725"
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                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:219732"
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AA849009.1 GI:2936549
                                                                                                                                                                                                                                                                                                                                                                    Bex="male"
                  Contact: Wilson RK
                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity
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Rattus sp.
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Missurcoulds Butheria; Rodentia; Sciurognath; Muridae; Mutenina; Markaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 466)

I (bases 1 to 466)

Nikaido; I., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido; I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Schriml, L.M., Ranaphin, A., Matuda, H., Batsel, W., Blake, J.A., Bradt, D., Bult, C., Corbani, L.E., Cousine, S., Datal, E. Dragani, T.A., Chothia, C., Corbani, L.E., Cousine, S., Dalla, E., Dragani, T.A., Gustincich, S., Hirokawa, N., Jackson, I.J., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Madlott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Ravasi, T., Reed, J.C., Red, J.G., Rend, J.G., Ramachandran, S., Ravasi, T., Rahenaka, Y., Pohtius, J.U., Oli, D., Kanaghanima, T., Rakenaka, Y., Pillait, R., Pohtius, J.U., Oli, D., Wardo, M., Schneider, C., Rend, D.J., Radalse, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlseted, J., Shingka, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yanayi, Y., Markawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotania, P., Hayasu, J., Maraki, T., Waki, K., Kawai, J., Anawa, K., Shinagawa, R., Yasawa, I., Watanabe, Y., Shinagawa, R., Yasawa, Y., Ruda, S., Hara, A., Hashizume, W., Imotania annotation of 60,770 full-length conse transcriptome based on functional annotation of 60,770 full-length conse
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                      /organism="Rattus sp."
/mol_type="mRNA"
/db_xref="%axon:10118"
/db_xref="teaxon:10118"
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/clone="RLUA196"
/clone="RLUA196"
/clone="forgan: lung; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: NotI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 74.4%; Score 18.6; DB 9; Length 391; Similarity 84.0%; Pred. No. 6.7e+02; 11; Conservative 0; Mismatches 4; Indels (
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                                                                                                  Location/Qualifiers
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BY514030.1 GI:26848409
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
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Best Local Similarity 84....
Thes 21; Conservative
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Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
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/strain="C57BL/6J"
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                                                                                  Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alizawa,K., Akimura,T., Arakawa,T., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakazume,N., Sasaxi,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramateu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDN libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1671-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-Dased methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 231-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osatco, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, bone marrow
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                                  Tel: 81-45-503-9222
Fax: 81-45-503-9216
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KEYWORDS
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Tissues were provided by Takashi Ishikawa ( Department of Surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome_res@gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakwa,T.,
Alzawa,K., Akimura,T., Arakwa,T., Itoh,M., Kawai,J., Konno,H.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,X.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/clone="1220028M18"
/cell_type="stroma_cell"
/clone_lib="RIKEN_full-length_enriched, stroma_cell"
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/organism="Mus musculus"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mans Müsculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 413)

Okazaki, Y. Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, H., Kriyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, H., Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, H., Rayosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, H., Batalov, S., Belsel, K., Blake, J., Brasic, V., Chothia, C., Gorbani, L. B., Cousine, S., Dalla, B., Dragani, T. A., Gughi, M., Ring, B.L., Konagaya, R., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Majott, D.R., Maltals, L., Marchinomi, L., Morkenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Pertea, G., Pertovsky, N., Pillai, R., Pontius, J.U., Oi, D., Famachandran, S., Ravasi, T., Reed, J.C., Reed, J.G., Ring, B.L., Kamachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sungisawa, M., Yang, L., Wahlestedt, C., Wang, Y., Watambe, Y., Wall, Y., Wanger, L., Wahlestedt, C., Wang, Y., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Xagawa, T., Myyazaki, A., Sabaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, R., and Hayashizaki, Y., Rogers, V., Analysis of the mouse transcriptome based on functional annotation of 60,700 cull. Length A. Dana
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                        BY573260 413 bp mRNA linear EST 15-DEC-2002
BY573260 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830301121 3', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                   Gaps
                                                                                   ö
74.4%; Score 18.6; DB 13; Length 411; 84.0%; Pred. No. 6.9e+02; ive 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA clone F830301121 3
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                                                                               21; Conservative
Query Match
Best Local Similarity
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SOURCE

COMMENT

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Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Musicaes 1 to 414)

Okazaki,Y., Furuno,M., Saito,R., Suzuki,H., Yamanaka,I.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyoswa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Schonbach,C., Gojobori,T., Baldarali,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackehbush,J., Schriml,L.M., Kanapin,A., Mateuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,L.J., Yarvis,E.D., Kanagaya,A.,
Kuwochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Ravasi,T., Reed,J.C., Reed,D.G., Reid,D.G., Stimmada,K.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomta,M.,
Verardo,R., Wapner,L., Wahlested,C., Wanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
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                                                                                                                                                                                Computer-based methods for the mouse full-length cDNA construction of a neryfologedia: real-time sequence clustering for construction of a nonreadundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration of Experimental Animal Research in Riken.
prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
KIKKN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 6.9e+02;
0; Mismatches 4; Indels 0:
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/clone="F830301121"
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/strain="NOD"
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84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY513444
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DEFINITION
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URL:http://genome.gsc.riken.go.jp,
Alzawa,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Arakawa,T., Itoh,M., Kawai,J., Konno,H.,
Hirozane,T., Imotani,K., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,T. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1610 (2000)
            Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shogars, J., Birney, E. and Hayashizaki, W., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissues were provided by David A. Hume ( Depts. of Biochemistry
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/clone_lib="RIKEN full-length enriched, bone marrow
Konno, H., Nakamura, M.,
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Pred. No. 6.9e+02;
0; Mismatches 4;
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Hayatsu, N., Hirozane-Kishikawa, T.,
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/clone="1830148K22"
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/strain="C57BL/6J"
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Similarity 84.0%;
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Mammalia, Eutheria; Kodentia; Sciurognathi; Muridae; Murinae; Murinae; Mammalia; Eutheria; Kodentia; Sciurognathi; Muridae; Murinae; Musado, T., Daseb I to 417)

Nikaido, T., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Ouackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchiconni, L., Merchiconi, J.U., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Pertea, G., Pertea, G., Pertea, G., Pertovsky, N., Pillai, R., Pontius, J.U., Oil, D., Kamachandran, S., Ravasi, T., Reed, J.C., Red, D.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Taylor, M.S., Taylor, M., Sato, K., Mangar, Y., Maranbe, Y., Waranbe, Y., Wang, Y., Wang, Y., Waranbe, Y., Yang, L., Wahlestedt, C., Wang, Y., Waranbe, Y., Hayatsu, N., Hirozane-Kishikawa, T., Yang, K., Yang, Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, K., Shiraki, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Ang, D., Sasaki, M., Bandyasa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Andyasis of the mouse transcriptome based on functional annotation of 60,770 full-lengthe construction of environment of construction of construction
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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URL:http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Itoh, M., Kawai, J., Konno, H.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
BY503440 RIKEN full-length enriched, bone marrow macrophage Musmusculus cDNA clone I830081H09 3', mRNA sequence.
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RIKEN integrated sequence analysis (RISA) system--384-format
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prepare mouse tissues.

EST 14-DEC-2002

linear

mRNA

417 bp

BY503440

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 418) Piao, Y. Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C0618D02-3 NIA Mouse Trophoblast Stem Cell cDNA Library (Long) Mus musculus cDNA clone NIA:C0618D02 IMAGE:30021925 3', mRNA sequence. BM207812
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitolology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
Sand Casell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: Co618 row: D column: 02
Seg primer: -21M13 Forward
High quality sequence stop: 418
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/clone lib="RIKEN full-length enriched, bone marrow
macrophage"
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/organie="Mus musculus"
/mol_type="mRNA"
/strain="B5/EGFP transgenic_ICR mice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="NIA:C0618D02 IMAGE:30021925"
/tissue type="Trophoblast stem cell"
/dev stage="3.5-dpc"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.6; DB 13;
Pred. No. 6.9e+02;
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                               tissue type="bone marrow"
                                                                                                                                                                                   organism="Mus musculus"
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/etrain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="1830081H09"
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4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-5. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation maxture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gow/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded codna were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by Yulan Piao (NIA)."
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                                                                                                                                                                                                                                                                                                                                Invitrogen:
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Best Local Similarity
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Search completed: March 25, 2004, 00:13:50 Job time: 1222.13 secs

394 AACCACCTTAGTTAGATAATCTTTT 370

Matches

à 셤

ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic Run on:

March 24, 2004, 21:53:36; Search time 906.607 Seconds (without alignments) 1960.127 Million cell updates/sec

US-09-889-611A-60\_COPY\_2\_42 Title: Perfect score:

1 gaatgaactacataacaacc.........ccttagtcagatactactt 41 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues Searched:

6940544

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

em\_ro:\* em\_sts:\* em\_un:\* em\_vi:\* em\_ntg\_hum:\* 9b ba:\*
9b htg:\*
9b on:\*
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em fun:\* em pat:\* #: m em om:\* em\_ph:\* em\_ov:\*  Pred. No. is the number of results predicted by chance to have a

em\_sy:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

em htg\_inv:\*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	uo	Ношо	Homo	Homo
	Description		AC072051 Homo sap	AC027524 Homo
	UI	AF234618	39.4 96.1 157284 9 AC072051	AC027524
	DB	9	Q	~
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### ALIGNMENTS

AF13461B 4229 bp DNA linear PRI 29-MAR-Homo sapiens megsin gene, promoter region and partial sequence. AF234618 AF234618.2 GI:19808130 RESULT 1
AF234618
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

PRI 29-MAR-2002

Homo sapiens (human) Homo sapiens ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4229)
Miyata,T., Nangaku,M., Inagi,R. and Kurokawa,K.
Transcriptional regulation of a mesangium-predominant gene, megsin Unpublished

FEATURES

ORIGIN

TITLE

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Submitted (07-JUN-2000) Whitehead Institute/MIT Center for Genome
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Web site: http://www-seq.wi.mit.edu
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/db xref="taxon:9606"
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Center clone name: 79_D_2
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JOURNAL
                                                     REFERENCE
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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2 (bases 1 to 4229)
Miyata T., Nangaku, M., Inagi, R. and Kurokawa, K.
Miyata T., Nangaku, M., Inagi, R. and Kurokawa, K.
Direct Submission
Submitted (15-FEB-2000) Institute of Medical Sciences and
Department of Internal Medicine, Tokai University School of
Medicine, Bohseidai, Isehara, Kanagawa 259-1193, Japan
3 (bases 1 to 4229)
Trani R. and Kurokawa, K.
                                                                                                                                                                                               Miyata,T., Nangaku,M., Inagi,R. and Kurokawa,K.
Direct Submission
Submission
Submission
Department of Internal Medicine, Tokai University School of
Medicine, Bohseidai, Isehara, Kanagawa 259-1193, Japan
Sequence update by submitter
On Mar 29, 2002 this sequence version replaced gi:18000453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

96.1%; Score 39.4; DB 9; Length 4229;
Best Local Similarity 97.6%; Pred. No. 7.4e-05;
Matches 40; Conservative 0; Mismatches 1; Indels 0;
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-79D21
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/product="megsin"
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/map="18q21.3"
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COMMENT
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KEYWORDS

LOCUS

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Direct Summission

Direct Summission

Direct Summission

Submitted (157284)

E (bases 1 to 157284)

E inton, 2. Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N. Bastien, V. Boquslavkiy, L. Boukhgalter, B., Camperian, Y. Callane, V. Colline, S., Collymore, A., Cooke, P., Darellano, K., Dewar K., Diaz, J. S., Dodge, S., Faro, S., Cooke, P., Dearellano, K., Dewar K., Diaz, J. S., Dodge, S., Faro, S., Gord, S., Gordette, M., Grana, J., Grand, Pleir Jenson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, E., Macdonald, P., Major, J., Marquis, N., Matthews, C., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Connor, V., Devine, R., Najor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Connor, P., O'Connor, V., Parger, R., Rieback, M., Riley, R., Schauer, S., Schuback, R., Seman, S., Severy, P., Spencer, B., Schaner, S., Theodore, J., Seaman, S., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Stansen, S., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Viel, R., 
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 157284)

3 (bases 1 to 157284)

3 (bases 1 to 157284)

5 Birten, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B. Borna, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Govette, M., Graham, L., Grand Plerre, M., Illev, I., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Lakocque, K., Lawazares, R., Landers, T., Lehoczky, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, J., Marthews, C., Macdonald, P., Major, T., O'Donnell, P., O'Connor, Y., Bange, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N. Strauss, N., Subramanian, A., Travis, N., Travis, N., Travers, Wulson, B., Wu, X., Wyann, D., Ye, W.J., Young, G., Subramanian, A., and Zody, M., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Travis, C., March, C., March, C., March, C., March, C., March, C., Milson, B., Wu, X., Warn, D., Ye, W.J., Young, G., Subrisson, M., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Travis, C., March, A., March, A., March, C., March, C., March, A., March, A., March, C., March, C., March, A., March, A
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------ Project Information
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ALE Uppublished

Chases 1 to 189092)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Baetlen, V., Beda, F., Bodukgalter, B., Bricket, G., Bricket, G., Bracket, G., Bracket, G., Bodukgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Colymore, A., Caoke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glude, S., Goyette, M., Graham, L., Kartas, J., Landers, T., Lehoczky, J., Howland, J.C., Iliev, I., Johnson, K., Jones, C., Kann, L., Kartas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McGonald, P., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McGonald, P., Marquis, N., McZarthy, M., McEwan, P., McGurk, A., McGonald, P., Berre, R., Lieu, C., Follara, T., Molver, J., Peterson, K., Pierre, N., Fisani, C., Pollara, Y., Naymon, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tajanas, J., Tarrell, A., Travers, M., Trigillo, J., Vassillev, H., Vlel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M. Trigillo, J., Vassillev, H., Vlel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M. 2ainoun, J., Zimmer, A. and Zody, M. 2ainoun, J., Zimmer, A. and Zody, M. 2ainoun, J., Zimmer, S., Barna, C., Jander, E., Ali, A., Allen, N., Alber, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Linton, L., Boguslavkiy, L., Boukhgalter, B., Stown, A., Camarata, J., Campopiano, A., Chang, J.,
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1 (bases 1 to 189092)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-317G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC027524 189092 bp DNA linear HTG 27-MAR-;
Homo sapiens chromosome 18 clone RP11-317G1 map 18, 3 unordered
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens (human)
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TITLE
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AUTHORS
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AC027524
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AX346917.1 GI:18494803

KEYWORDS

ERSION

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Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farzelara, P., FirzGerald, M., Firzhoy, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, M., Hagos, B., Horton, L., Hulme, W., Iliev, I., LaRoque, K., Johnson, R., Jones, C., Kamat, A., Karates, A., Kells, C., LaRoque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Nicol, R., Norbu, C., Netta, R., Rieback, M., Riley, R., Riee, C., Rolli, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Strauss, N., Stansennian, A., Talams, J., Testaye, S., Theodore, J., Topham, K., Travis, N., Trigilio, J., Ve, W.J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 1, 2002 this sequence version replaced gi:11990731.
All repeats were idea using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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85759: gap of 100 bp
163014: contig of 77255 bp in length
163114: gap of 100 bp
189092: contig of 25978 bp in length.
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Best Local Similarity 97.6%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.

E. (bases 1 to 207510)

Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Engle, J., Granite, S., Guun, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R.,
Karlins, E., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C.,
Maskeri, B., McDowell, J., Mullikin, J.C., Paquirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Reddix-Duque, N., Schanler, K.,
Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and
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Otolemur garnettii clone CH256-273K16, WORKING DRAFT SEQUENCE, 2
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-DEC-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                           Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1988 03-JAN-2002;
Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%; Score 33.6; DB 6; Length 6182; 90.0%; Pred. No. 0.014; tive 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1310 AATAAACTACATAACAACCACCTTAATCAAATACTATTT 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: NIH Intramural Sequencing Center

    .6182
/organism="synthetic construct"

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Otolemur garnettii (small-eared galago)
Otolemur garnettii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NISC Comparative Sequencing Initiative Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 273K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: fhy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Center
                                                                                                                                                                                                                            Location/Qualifiers
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                                                     artificial sequences.
synthetic construct
synthetic construct
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nes 36; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                          ORGANISM
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AUTHORS
                                                                                                                                                                      JOURNAL
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                                                                                                              AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                             REFERENCE
                                                                                                                                                                                                                               FEATURES
                                                                                                                                           TITLE
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PAT 01-FEB-2002

linear

DNA

6182 bp

AX346917

LOCUS

ACCESSION

RESULT 4 AX346917/c

Sequence 1988 from Patent W00200928. AX346917

Gaps

..

1; Indels

0; Mismatches

40; Conservative

Matches

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E. Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Albbrooks, S., Amin, A., Angulano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Blankenburg, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Checko, J., Chavez, D., Chen, G., Chen, R., Chen, T., Chen, T., Chen, G., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Dapper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Rugene, C., Evans, C. A., Foster, M., Gabisi, A., Ganta, R., Garcia, A., Garcia, M., Guerra, W.,

Gebregoorgis, R., Gabisi, A., Ganta, R., Gardy, M., Guerra, W.,

Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
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Rattus norvegicus 13 BAC CH230-127N19 (Children's Hospital Oakland
Research Institute) complete sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                             Insert size: 207410; sum-of-contigs
Quality coverage: 14.36x in Q20 bases; agarose-fp
Quality coverage: 15.10x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.7%; Score 29.4; DB 2; Length 207510; Best Local Similarity 84.6%; Pred. No. 0.44; Matches 33; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 38181: contig of 38181 bp in length

38182 38281: gap of unknown length

38282 207510: contig of 169229 bp in length.

Location/Qualifiers

1. .207510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Otolemur garnettii"
| mol Lype="genomic DNA"
| db xref="taxon:30611"
| clone="CH256-273X16"
Insert size: 218000; agarose-fp
Insert size: 207410; sum-of-cont
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38282. 207510
/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="CH256"
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Harrandez, Hames, S., Hadwes, A., Handerson, N., Harrandez, J., Harrandez, S., Hawes, S., Handen, S.L., Hodgson, A., Hogues, M., Jollins, B., Howells, S., Halyk, S.L., Hodgson, A., Hogues, M., Jolkson, L., Jacokson, J., Liu, M., Liu, Y., London, P., Loyan, J., Lewis, L., Liz, Z., Liu, J., Liu, M., Liu, Y., London, P., Loyagacre, S., Lopez, J., Liu, M., Liu, Y., London, P., Loyagacre, S., Lopez, J., Liu, M., Mahindartne, M., Mahmoud, M., Malloy, K., Margun, M., Mangun, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Minja, B., Mapua, P., Martin, K., Martin, R., Mannidas, M., Montenall, T., Meenen, E., Milosavijevic, A., Montenall, T., Manner, B., Minja, B., Montenayor, J., Naoce, S., Morgan, M., Morris, K., Martin, R., Mannidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Noris, S., Masternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Perez, A., Perez, A., Regier, M.A., Reigh, R., Rellly, B., Rellly, M., Ren, Y., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Riggs, F., Rives, C., Rodfey, T., Rojas, A., Song, X.-Z., Socrile, R., Shen, H., Shetty, J., Shvattsbeyn, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Warten, R., Wei, X., White, P., Wall, B., Wang, G., Wang, S., Warten, R., Wei, X., White, P., Walls, R., Wang, G., Wang, S., Wang, C., Yen, J., Yoon, L., Walley, R., Wang, G., Wang, S., Wang, C., Yen, Soder, S., Shen, H., Wooley, R., Wang, G., Wang, S., Wang, S., Wang, C., Yen, Soder, S., Dunn, D., Von Niederhausern, A., Weiss, R., Smith, D.R., Phun, D., Von Niederhausern, A., Weiss, R., Smith, D.R., Dunn, D., Von Niederhausern, A., Weiss, R., Smith, B., A., Smith, B., A., Smith, S., Wang, G., Wang, S., Shen, W., Savery, S., Shen, H., Walley, R., Wang, G., Wang, S., Shen, W., Savery, S., Shen, J., Yon, L., Yoon, V., Willey, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (07-JUN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 7, 2003 this sequence version replaced gi:30521373.
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
it will be indicated in the annotation.
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Submitted (25-NOV-2001) Human Genome Sequencing Center, Department
Submitted (25-NOV-2001) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 199669)
Rat Genome Sequencing Consortium.
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4 (Dases 1 to 199669)
           ., Henderson, N., Hernandez, J.,
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/db_xref="taxon:10116"
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Нагvey,Y., Havlak,P., Наwев,A.
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/rpt family="tx2_3"
5760. .5861
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5862. .6447
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6522. .6886
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6611. .6938
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Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/rpt_family="(TC)n"
complement(33409. .33631)
/rpt_family="Limbs"
complement(33705. .33796)
/rpt_family="Limbs"
                                                                                                                                                                                                                                                                                                                                                                              family="ID_Rn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      omplement (26236. .26625)
rpt_family="Lx_3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Mrc-int"
complement(29316..29403)
/rpt_family="ID_Rn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich"
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/rpt_family="L1"
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>mplement (30346. .30535)
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31316. 31418 "MTC-int"

31316. 31418 "MTC-int"

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31450. 31883

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31999. 31998

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                                         Complement (7044. .7089)
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family="(TA)n"
                                                                                                                                                                                                                                                                                                                        . .13075
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6939. .7037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="Lx_3"
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                                                                                                                                                                                                                                                                                                                                                                                   complement (17119.
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                                                                                                        complement (7190
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Rattus norvegicus clone CH230-318J10, *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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complement(39114..39170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="MTD"
complement(39168. .39315)
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36664 .36875
/rpt_family-"LIMA6"
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35209. 35296
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   33877. .34086
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Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USB.

To Rolecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USB.

The sequence in this sequence version replaced gi:22759157.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence cands. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequence in the feature and the sequence and se
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Wa, J.,
Maheshwari, M., Mahindartne, M., Martin, R., Martinez, E.,
Maheshwari, M., Mahindartne, M., Martin, R., Martinez, E.,
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Direct Submission

Submitted (09-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 219071)
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 194595 bases at least Q40
Consensus quality: 196491 bases at least Q30
Consensus quality: 200795 bases at least Q30
Estimated insert size: 200795 bases at least Q30
Betimated insert size: 200795 bases; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Mus musculus BAC clone RP24-560M23 from chromosome 1, complete
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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.8%; Score 28.2; DB 2; Length 219071; Best Local Similarity 80.5%; Pred. No. 1.3; Matches 33; Conservative 0; Mismatches 8; Indels 0;
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                                                                                                                  1 217199: contig of 217199 bp in length 217200 217200 2999: gap of unknown length 217300 219071: contig of 1772 bp in length. Location/Qualifiers
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    .6182
/organism="synthetic construct"

                                                                                                                                                                                                                                        organism="Rattus norvegicus"
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Epigenomics AG (DE)
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2X346916
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152568 .153448
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ORGANISM

SOURCE

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COMMENT

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                                                      'mol_type="genomic DNA"
'db_xref="taxon:10090"
'chromosome="1"
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                                                                                                                                                           clone lib="RPCI-24"
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3801. .13978
                                                                                                                                           clone="RP24-560M23"
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/rpt_family="ERV1"
15664. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /501 .7597
/rpt_family="MaLR"
7663 R1EA
location/Qualifiers
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2864. .13008
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/rpt_family="L1"
11519. 11625
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/rpt_family="L1"
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0108. .10198
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.8013. .18607
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7455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections ence, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-UUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (Dases 1 to 121538)
MCPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-OCT-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 6 (bases 1 to 121538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 121538) Mang,C., Haakenson,W. and Haglund,K.
The sequence of Mus musculus BAC clone RP24-560M23
Uppublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-MAR-2003) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- Summary Statistics
Center project name: M_BB0560M23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 121538)
                                                                                                                                                                                                                                                                                                             Unpublished (2001)
3 (Dases I to 121538)
MCPharson, J. D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                       Sequencing of Mus musculus
                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genome.wustl.edu
                                       AC129295.4 GI:37651860
                                                                                                                                                                                                                                                  (bases 1 to 121538)
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                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R.K.
  sequence.
                                                                                                                                                                                                                                                                    Wilson, R
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rpt\_family="B2" 9909. .19963

repeat\_region repeat\_region repeat\_region repeat\_region

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

SOURCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone.

/rpt\_family="MaLR"

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 20084)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-70H12
              REFERENCE
AUTHORS
                                        TITLE
JOURNAL
REFERENCE
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JOURNAL
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45732. 46123
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6. .38239
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/rpt_family="Malk"
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40638. .41045
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (26-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 26, 2003 this sequence version replaced gi:2875018
All repeats were identified using Repeatmasker:
Smit, A.F.A. & Green, P. (1996-1997)
Herrin, Menson Manna, Manna
                                                                     Exercises 1 to 200844)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, T., Boour, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dedrellano, K., Dewar, T., Collymore, A., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Farreira, P., FitzGerald, M., Cando-Pierre, N., Hagos, B., Horton, L., Hulme, M., Illev, I., Johnson, F., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mangay, V., Murphy, T., Naylor, J., Neneus, L., Mihova, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phurkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Hilson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WBR
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Contact: sequence_submissions@genome.wi.mit.edu
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Unpublished
2 (bases 1 to 200844)
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Gaps

AC134414 20-FEB-2003 Mus musculus clone RP24-70H12, WORKING DRAFT SEQUENCE, 13 unordered

AC134414

RESULT 10 AC134414/c DEFINITION pieces.

1 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 41

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Matches

Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AC134414 AC134414.3 GI:28565730 HTG: HTGS PHASE1; HTGS DRAFT. Mus musculus (house mouse)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                              NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
Quality coverage: 8.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1317 101416: gap of 100 bp

417 120870: contig of 19454 bp in length

1871 120870: gap of 100 bp

1871 120870: gap of 100 bp

1871 145380: contig of 24410 bp in length

1381 145480: gap of 100 bp

1481 174041: contig of 28561 bp in length

174141: gap of 100 bp

174141: gap of 100 bp

174141: gap of 100 bp

1752 200844: contig of 26703 bp in length.
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clone\_end:T7

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AB Unpublished

Birren, B. Lintcon, L. Nubbaum, C., Lander, E., Ali, A., Allen, N.,

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Zainoun, J., Subramian, A., Lalamas, J., Teefays, S., Thedore, J.,

Nobmitted (13-EB-2002) Whitehead Institute/WIT Center for Genome

M. Direct Submission

M. Direct Submission

M. Direct Submission

M. Direct Submission

Submistred, M., Wilson, B., Wull, Wayne, C., Morman, M., Gooke, P., Boom, T., Boukhgalter, B.,

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Mus musculus clone RP23-309J17, WORKING DRAFT SEQUENCE, 7 ordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                          Gaps
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61.0%; Score 25; DB 2; Length 200: 75.6%; Pred. No. 24; 10; Indels ive 0; Mismatches 10; Indels
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Mus musculus (house mouse)
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-309J17
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                                Similarity
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REFERENCE
AUTHORS
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JOURNAL
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This sequence will be replaced

* This sequence as soon as it is available and

* the finished sequence as soon as it is available and

* the accession number will be preserved.

1 65944: contig of 6594 bp in length

66045: 66044: gap of 100 bp

69783: 73657: contig of 3638 bp in length

69783: 73657: contig of 3875 bp in length

73758: 73757: gap of 100 bp

73758: 134380: gap of 100 bp

134481: 162491: contig of 28011 bp in length

162492: 200818: gap of 100 bp

162592: 200818: gap of 100 bp

200819: 200818: gap of 100 bp

200819: 200818: gap of 100 bp

200819: 213457: contig of 12539 bp in length
                                                                                                                                                                                                                                   Center clone name: 309 J.1.

Center clone name: 309 J.1.

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 212725 bases at least Q30
Consensus quality: 212828 bases at least Q30
Insert size: 210000; agarose-fp
Insert size: 212857; sum-of-contigs
Quality coverage: 11.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP23-309J17"
/clone_lib="RPCI-23 Female Mouse BAC"
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69783, ,73657
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clone_end:SP6
vector_side:left"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                        Center project name: L22620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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vector_side:right"
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                                                                                                                                             Center code: WIBR
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only a small overlap as described above only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, GMSSRROT; Tr:, TREMBL; Wo:, WORNPEP; Information on the WORNPEP database can be found at.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AL672023 160615 bp DNA linear ROD 26-JUN-2002 Mouse DNA sequence from clone RP23-339019 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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For further details see http://www.chori.org/bacpac/home.htm VBCTOR: pBACe3.6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 27, 2002 this sequence version replaced gi:21531223.
                                                                                                                Gaps
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0
                                 61.0%; Score 25; DB 2; Length 213457; 75.6%; Pred. No. 24; Live 0; Mismatches 10; Indels 0
                                                                                                                                                                                                                                                        58385 GAATAAACCACAGAATTAAGACCTIGGICAAATATTACTTI 58345
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Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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Mus musculus
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Best Local Similarity 75...
Best 10cas 31; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Submitted (13.MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@Akfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686G0837) is available at the RZDD in Berlin.
Please contact the RZDD: Reseaucrentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzgd.de Further
information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="DKFZp686G0837"
/clone="DKFZp686G0837"
/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sfi; host
DH10B; Sitem SfilA + SfilB"
/dev_stage="adult"
3455..3440
                                                                                                HSM804835 3473 bp mRNA linear PRI 13-MAY-2003
Homo sapiens mRNA; cDNA DKFZp686G0837 (from clone DKFZp686G0837).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Sequence 101 from Patent WO0168912.
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.5%; Score 24; DB 6; Length 5276; 75.0%; Pred. No. 80; 10: Indels 10; Indels
                                                              Score 24; DB 6; Length 5276;
Pred. No. 80;
                                                                                                                0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                      544 AATTACCTACATAACACTCATAACTCAAATTCTACATT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 AATTACCTACATAACAAACTCATAACTCAAATTCTACATT 505
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                                                                                                                                                             2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                    AX345728 5276 bp I
Sequence 799 from Patent WO0200928.
AX345728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March 24, 2004, 23:01:31 Job time: 911.607 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       AX345728.1 GI:18493614
                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic construct
synthetic construct
artificial sequences.
                                                                  58.5%;
75.0%;
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                                                                                                                30; Conservative
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Best Local Similarity
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13.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

March 24, 2004, 18:56:32 ; Search time 214.674 Seconds
 (without alignments)
 811.351 Million cell updates/sec Run on:

US-09-889-611A-60\_COPY\_2\_42

1 gaatgaactacataacaacc.........ccttagtcagatactacttt 41 Perfect score: Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1980s:\* genesequ1990s:\* genesequ2000s:\* genesequ2001as:\* genesequ2001as:\* genesequ2003s:\* genesequ2003as:\* geneseqn2003bs:\* N Geneseq 29Jan04:\* geneseqn2003cs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

SUMMARIES

## \* Ouerv

Description	Aaa71435 Himan med	Human		Aaa71449 Human meg	_	Human	Human	Aas46379 Tumour su	Abl32826 Human imm		Adc92907 E. faeciū	Abl32899 Human imm		Abl32720 Human imm	Abk34986 Human CDN	Abl13848 Drosophil	_		Abk38088 cDNA enco	Acal0417 Human lun			Aas72599 DNA encod	
ID	AAA71435	AAA71434	ABL34015	AAA71449	AAA71448	AAA71453	ABL34014	AAS46379	ABL32826	AAA71452	ADC92907	ABL32899	ABK39985	ABL32720	ABK34986	ABL13848	AAS94755	AAF68177	ABK38088	ACA10417	ABX99368	ADE72151	AAS72599	
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Match Length DB	1431	128	6182	30	30	25	6182	5276	5276	23	1380	5204	11052	6503	2222	3561	6568	1265	1265	1265	1265	1265	1350	
Match	100.0	97.6	82.0	73.2	73.2	61.0	61.0	58.5	58.5	56.1	54.6	54.6	54.6	53.7	53.2	53.2	53.2	52.7	52.7	52.7	52.7	52.7	52.7	
Score	41	40	33.6	30	30	25	25	24	24	23	22.4	22.4	22.4	22	21.8	21.8	21.8	21.6	21.6	21.6	21.6	21.6	21.6	
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Abl32272 Human imm		Abls6202 AmBPV gen		Aat84004 DNA encod	Abt14864 Pathogen	Acf74277 Staphyloc	Adb62739 Human cDN	Ada89881 Staphyloc	Abx13873 cDNA enco		Ada89856 Staphyloc		Abl03172 Drosophil	Aaq55133 Staphyloc	Aca29071 Prokaryot	Abl32921 Human imm	Abk34027 Human DNA	Ada20447 Prostate	Ada84254 Human ren	Aba20517 Human ner	Abl32991 Human imm
ABL32272	ABL55639	ABL56202	ABL29244	AAT84004	ABT14864	ACF74277	ADB62739	ADA89881	ABX13873	ABK13619	ADA89856	ACA25060	ABL03172	AAQ55133	ACA29071	ABL32921	ABK34027	ADA20447	ADA84254	ABA20517	ABL32991
φ	φ	ø	4	N	7	7	σ	~	9	ø	7	7	4	~	7	9	ø	7	7	'n	9
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52.7	52.2	52.2	52.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.2	50.7	50.7	50.7	50.7	50.7	50.7	50.7
21.6	21.4	21.4	21.4	21	21	21	21	21	21	21	21	21	21	21	20.8	20.8	20.8	20.8	20.8	20.8	20.8
24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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BP.
                       AAA71435 standard; DNA; 1431
RESULT 1
             AAA71435
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AAA71435;

(first entry) 01-DEC-2000 Human megsin promoter fragment DNA.

Promoter; megsin; human; protein isolation; screening. ss.

Homo sapiens.

WO200043528-A1.

25-JAN-2000; 2000WO-JP000350. 27-JUL-2000.

99JP-00015667. (KURO/) KUROKAWA K. (MIYA/) MIYATA T. 25-JAN-1999; 

Miyata T;

WPI; 2000-543257/49.

DNA for promoter region of megsin useful for screening proteins

Disclosure; Fig 2; 45pp; Japanese.

This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (I) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (especially transcription factors). This sequence represents a fragment of the human megsin promoter which is

Sequence 1431 BP; 466 A; 266 C; 303 G; 394 T; 0 U; 2 Other;

Gарв 0; Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 41; Conservative 0; Mismatches 0; Indels (

; 0

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AAA71434

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acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
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                                                                                                                                                          02-JUL-2001; 2001WO-EP007537.
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Conservative
                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                        WPI; 2002-130909/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                               WO200200928-A2.
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                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region having part or all of a specific base sequence. The invention also describes (1) a vector containing (1); (2) a cell transformed by the above vector; and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors). This sequence represents the human megsin promoter which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel DNA sequence (I) representing a promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease, cytosine methylation, antiasthmatic, antiarteriosclerotic; antianaemic; cytostatic; noctropic; eneroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarharitic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA for promoter region of megsin useful for screening proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match 97.6%; Score 40; DB 3; Length 128; Local Similarity 100.0%; Pred. No. 4.6e-06; les 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Promoter; megsin; human; protein isolation; screening. ss.
                                    1303 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 128 BP; 44 A; 29 C; 24 G; 29 T; 0 U; 2 Other;
                     41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 1988.
                    1 GAATGAACTACATAACAACCACCTTAGICAGATACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT
                                                                                                                                                                                                                             Human megsin promoter fragment DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 32; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL34015 standard; DNA; 6182 BP
                                                                                                                                ВЪ
                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000; 2000WO-JP000350.
                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-00015667
                                                                                                                               AAA71434 Btandard; DNA; 128
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                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-543257/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KURO/) KUROKAWA K.
MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                                                                          WO200043528-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1999;
                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                         27-JUL-2000.
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                                                                                                                                                               AAA71434;
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ABL34015/c

RESULT 3

Matches

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid theumania, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.6; DB 6; Length 6182;
Pred. No. 0.0028;
                                                                                                                                                                           Claim 1; SEQ ID NO 1988; 32pp + Sequence Listing; German.
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                                                                              This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (1); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (sepecially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (1); (2) a cell transformed by the above vector; and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; meggin; human; protein isolation; screening. PCR primer; ss
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                                 DNA for promoter region of megsin useful for screening proteins.
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73.2%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                   DB 3; Length 30; 0.031;
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                                                                                                                                                                             Sequence 30 BP; 12 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                           Human megsin promoter PCR primer SEQ ID NO: 15.
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                                                                                                                                                                                                   73.2%; Score 30; 100.0%; Pred. No.
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                                                         Example 5; Page 40; 45pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                    AAA71448 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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             WPI; 2000-543257/49
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(MIYA/) MIYATA T.
                                                                                                                                                                                                                Local Similarity
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This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (I) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (sepecially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
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1 Similarity 100.0%; Pred. No. 2.7;
25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 8 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Human megsin promoter PCR primer SEQ ID NO: 20.
                               1 AATGAACTACATAACAACCACCTTAGTCAG 30
2 AATGAACTACATAACAACCACCTTAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AACCACCTTAGTCAGATACTACTTT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AACCACCTTAGTCAGATACTACTTT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 42; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000WO-JP000350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-00015667,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL34014 standard; DNA; 6182
                                                                                                                                                                                                          AAA71453 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                   01-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-543257/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KURO/) KUROKAWA K. (MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200043528-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miyata T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                      AAA71453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL34014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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IID ABL3
XX ABL3
XX AC ABL3
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XX ATL1
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Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-602752/68.

(EPIG-) EPIGENOMICS AG.

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                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful idiagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour suppressor gene derived chemically modified sequence #101.
                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                           Sequence 6182 BP; 1929 A; 37 C; 1260 G; 2956 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.0%; Score 25; DB 6; Length 6182; Best Local Similarity 75.6%; Pred. No. 6.6; Matches 31; Conservative 0; Mismatches 10: Indels
                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1987; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 41
                                                                                                                                                                Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS46379 standard; DNA; 5276 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000DE-01019058.
; 2000DE-01019173.
; 2000DE-01032529.
; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2001; 2001WO-EP002955.
                                                                                        02-JUL-2001; 2001WO-EP007537.
                                                                                                            30-JUN-2000; 2000DE-01032529
                                                                                                                       01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2001 (first entry)
                                                                                                                                                               Olek A, Piepenbrock C,
                                                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                  WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200168912-A2.
                                                 WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                              Homo gapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2000;
                                                                                                                                                                                                                           methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-2001
                                                                    03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            4872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS46379;
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes. Laving a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid—oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single culeicated polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cliseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters with differences serving as basis for daryons and an expensive sequence is one of the 533 genomic sequences darients. The present sequence is one of the 533 genomic sequences dary for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulaant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 4; Length 5276; Pred. No. 16; O; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 AATTACCTACATAACAAACTCATAACTCAAATTCTACATT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT
                                                                                                                                                                                Claim 1; SEQ ID NO 101; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL32826 standard; DNA; 5276 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 58.5%;
1 Similarity 75.0%;
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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AAA71434-A71469 represent PCR primers used in the method described in the

invention

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This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (1); (2) a cell transformed by the above vector; and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors).
                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                           including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, ansemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoter; megsin; human; protein isolation; screening. PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA for promoter region of megain useful for screening proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5276 BP; 1546 A; 88 C; 1102 G; 2540 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 6; Length 5276;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 10; Indels
                                                                                                                                                                                                                           Claim 1; SEQ ID NO 799; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 AATTACCTACATAACAAACTCATAACTCAAATTCTACATT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human megsin promoter PCR primer SEQ ID NO: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 42; 45pp; Japanese.
                                                                                     Berlin K;
30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-00015667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2000; 2000WO-JP000350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA71452 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.5
Best Local Similarity 75.0
Matches 30; Conservative
                                                                                     Piepenbrock C,
                                                  (EPIG-) EPIGENOMICS AG.
                                                                                                                      WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-543257/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KURO/) KUROKAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MIYA/) MIYATA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200043528-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1999;
                                                                                                                                                                                            methylation.
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                                                                                 olek A,
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Gaps

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Enterococus faecium encoding an Enterococus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it. Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. uninary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid derived from Enterococcus faecium encoding a Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid derived from
                                                                                        56.1%; Score 23; DB 3; Length 23; 100.0%; Pred. No. 17; 0; Indels ive 0; Mismatches 0; Indels
                                                    Sequence 23 BP; 11 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the disclosed E. faecium nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 2534; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 B. faecium DNA sequence SEQ ID 2534.
                                                                                                                                                                    1 GAATGAACTACATAACAACCACC 23
                                                                                                                                                                                                     1 GAATGAACTACATAACAACCACC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                  ADC92907 standard; DNA; 1380 BP
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98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doucette-Stamm LA, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                             23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-799836/75
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADC96561,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6583275-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infection.
                                                                                                                                                                                                                                                                                                                                       ADC92907;
                                                                                                                               Matches
                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                ADC92907
                                                                                                                                                                                                                                                                                                                   SKKG
                                                                                                                                                                    à
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Sequence 1380 BP; 475 A; 213 C; 306 G; 386 T; 0 U; 0 Other;

Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.

Human chemically pretreated gene sequence #34 strand 1.

21-MAY-2002 (first entry)

ABK39985;

ABK39985 standard; DNA; 11052 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antintheumatic; antarticy ander; eye disease; arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epileps; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 5204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5204 BP; 1302 A; 79 C; 1119 G; 2704 T; 0 U; 0 Other;
DB 9; Length 1380;
                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulBant; ophthalmological;
Score 22.4; DB 9; Length 1 Pred. No. 55; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 872; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1180 AATAAAAACATTATAACTACCTTAAACAATTACAACTTT 1141
                                                                     1019 GATTGACCTACATCACAACCAAACCAAACAGATTCTCCTT 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                               40
                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 872,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT
                                              1 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.6%; Score 22.4; 72.5%; Pred. No. 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin K;
                                                                                                                                ABL32899 standard; DNA; 5204
                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP007537,
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-01032529, 01-SEP-2000; 2000DE-01043826.
 54.6%;
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Conservative
Query Match
Best Local Similarity 72.5
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                             WO200200928-A2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002.
                                                                                                                                                       ABL32899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                        RESULT 12
ABL32899/c
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New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.

Berlin K;

(EPIG-) EPIGENOMICS AG. Olek A, Piepenbrock C,

WPI; 2002-154757/20.

29-JUN-2001; 2001WO-EP007470. 30-JUN-2000; 2000DE-01032529. 01-SEP-2000; 2000DE-01043826.

Homo sapiens. WO200202806-A2.

LO-JAN-2002

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Claim 1; SEQ ID NO 67; 24pp; English.

The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes caseociated with pharmacogenomics according to one of the sequences of the caseociated with pharmacogenomics according), CTP11B1 (NM 000497), CTP3A3 (NM 001905), CTP11B1 (NM 0019079), CCLN (NM 00100776 and NM 019901, NM 019902, NM 019902, NM 019905, NM 019905, NM 019901, NM 019902, NM 019902, NM 019902, NM 019902, NM 019903, NM 019902, NM 019903, NM 019903, NM 019902, NM 019
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RESULT 14 ABL32720/c

RESULT 13 ABK39985/c autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.

Agostino MJ, Howes SH,

Clark HF, Fechtel K,

Gulukota K, Graham JR; WPI; 2002-179321/23.

29-MAR-2001; 2001WO-US010224. 06-APR-2000; 2000US-0195582P. (GEMY ) GENETICS INST INC

WO200177288-A2. Homo sapiens.

18-OCT-2001

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarthritic; antidabetic; antipsoriatic; antiantialidic antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6503 BP; 1561 A; 85 C; 1446 G; 3411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 53.7%; Score 22; DB 6; Length 6503; Local Similarity 73.7%; Pred. No. 1e+02; les 28; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 693; 32pp + Sequence Listing; German.
                                                                                                                  Human immune system associated gene SEQ ID NO: 693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AATGAACTACATAACAACCACTTAGTCAGATACTACT 39
ABL32720 standard; DNA; 6503 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                       WO200200928-A2
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation.
                                                                           26-MAR-2002
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a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the identification and isolation of full length conk and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating conditions (e.g. asthma). They are also useful for treating inflammatory disorders (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coaquiation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopolesis and for treating mysloid or lymphoid cell deficiencies. Sequences ABK34863-ABK35454 represent polymucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 592 polynucleotides which have been derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2037 GACTGAACTACACACCAAGGATCTTGTTCAAATACAAATGT 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.2%; Scc... No. 15... 70.7%; Pred. No. 15... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 130-131; 372pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Conservative
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Best Local Similarity
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Search completed: March 24, 2004, 22:28:26 Job time : 217.674 sec8

Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; asthma; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;

Human cDNA encoding secreted protein #124.

(first entry)

08-MAY-2002

ABK34986;

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Gaps

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509 AATAAAACACATAAAAATCACCATCGTCCTATATTACT 472

ABK34986 standard; cDNA; 2222

ABK34986/c

RESULT 15

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BX499268 DKFZp7791
BE539741 601061814
CA788473 AGENCOURT
AL317599 Tetraodon
                                                                 March 24, 2004, 21:57:32; Search time 1996.1 Seconds (without alignments) 613.370 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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                                             OM nucleic - nucleic search, using sw model
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BE539741
CA788473
CNS0521Y
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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Perfect score:
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BZ141244 CH230-257 CG156013 PUILP70TD CG431901 Bg49-T7 G CG431789 Bg110-T3 BJ624928 BJ624928 BJ096452 BJ096452 CA791463 AGENCOURT AQ302725 HS 3217 B	RECORDER DE SERVINE DE	CC552939 CH261-190 AK034567 Wus muscu BP020321 BP020321 BP024827 BP024827 BB269027 BB269027 BW116259 BW116259
BZ141244 CG156013 CG431901 CG431789 BJ624928 BJ096452 CA791463 AQ302725	AZISATION STATES OF THE STATES	CC252939 AK034567 BP020321 BP024827 BB269027 BW116259
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855 991 1018 1054 620 631 832 542		1330 1408 260 293 304 313
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ALIGNMENTS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKRZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.

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413 GCATATACTAAATAAGTTCCAGCTAAGTCAGGTACTACTT 452
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                                                                                          RESULT 3
CA788473
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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CNS0521Y
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KEYWORDS
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E 1 (bases 1 to 631)

NIH-MCC http://mgc.nci.nih.gov/.

Inpublished (1939)

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://mage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE539741 691 bp mRNA linear EST 09-AUG-2000 601061814F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3448443 5',
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                                                                                                                                                                                                                      /dev stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSportl_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="NIH MGC_10"
/note="Organ: cervix; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
  This clone (DKFZp77910544) is available at the RZPD in Berlin. Please contact the RZPP: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 523;
                                                                                                                                                                                                                                                                                                                                                        Query Match 58.5%; Score 24; DB 13; Length 52 Best Local Similarity 75.0%; Pred. No. 3.1e+02; Matches 30; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 GCATATACTAAATAAGTTCCAGCTAAGTCAGGTACTACTT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTT 40
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High quality sequence start: 15
High quality sequence stop: 635.
Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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ORGANISM
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AUTHORS
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BE539741
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KEYWORDS
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Linn at:
http://image.llnl.gov
Plate: LiAM11212 row: e column: 18
High quality sequence statt: 89
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CA788473 10306216 NICHD_XGC_OOI Xenopus laevis cDNA clone IMAGE:5079161 5', mRNA sequence.
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/note="Vector: pcMv-SPORT6; Site_1: Not1; Site_2: Sal1;
cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
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GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
Tetracdon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Percomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontoidea; Tetracdontidae; Tetracdon.
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae, Xenopus.
1 (bases 1 to 713)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
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                                                                                                                                                             CA788473.1 GI:26032557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
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Best Local Similarity
Matches 30; Conservat
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REFERENCE

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Gaps .**,** 

1 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTT 40

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Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plater. 257 row: B column: 15 Seg primer: SP6 Class: BAC ends.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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CoT selected genomic DNA library"
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/note="Vector: PTARBAC1.3; Site_1: Mbo1; Site_2: Mbo1;
CHORL-230 Rat (BN/SBNHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUIIP70TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0591L20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 23.4; DB 28; Length 73.2%; Pred. No. 5.5e+02; ive 0; Mismatches 11; Indels
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    .855 / Attus norvegicus"

                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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/db_xref="taxon:10116"
/clone="CH230-257B15"
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/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
Other GSSs: PUIIP70TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG156013
CG156013.1 GI:34046814
                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
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Class: sheared ends.
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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Jabo.S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shows,A., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Riggs,F., de Jong,P. and Fraser,C.M.
Uppublished (1999)
Other_GSSs: CH230-257B15.TV
Contact: Shaying Zhao
Department of Bukaryotic Genomics
Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
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9712 Medical Center Dr., Rockville, MD 20850, USA
TEL: 301 838 0200
Fax: 301 838 0208
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/lab_host="E. coli XLR Blue"
/clone_lib="Glomus intraradices Bgl II library (in pBK-CMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Mexico State University
BOX 30001, 3MLS, Las Cruces, NM 88003, USA
Tel: 505-646-3918
Fax: 505-646-6846
Fax: 505-646-6846
Faxil Folammers@rmsu.edu
Result of blastx search of NCBI non-redundant protein database, June 2003: No significant matches.
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/strain="DAOM 197198, Biosystematic Research Center,
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Bukaryota; Pungi; Glomeromycota; Glomerales;
Glomeracea; Glomus.
1 (bases 1 to 1018)
Lammers, P.J., Raryanaka, S., Rehrer, C. and Jun, J.
Genomic sequence from Glomus intraradices spore tissue
Unpublished (2003)
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    Length 991;
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Score 23.2; DB 29;
Pred. No. 6.6e+02;
0; Mismatches 8;
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                                                                             2 AATGAACTACATAACAACCACCTTAGTCAGATACTA 37
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/organism="Glomus intraradices"
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Location/Qualifiers
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CG431901.1 GI:34766767
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Query Match 56.6%;
Best Local Similarity 77.8%;
Matches 28; Conservative
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Class: plasmid ends
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/lab_host="E. coli XLR Blue"
/clone_lib="Glomus intraradices Bgl II library (in pBK-CMV
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Eukaryota; Fungi; Glomeromycota; Glomerales; Glomeraceae; Glomeraceae; Glomus.

1 (Dases I to 1054)

1 (Lases I to 1054)

1 (Lases I to 1054)

1 (Cases I to 1054)

1 (Cases I to 1054)

2 Genomic sequence from Glomus intraradices spore tissue

1 (Dupulished (2003)

2 Contact: Peter Lammers

New Mexico State University

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Tel: 505-646-3946

Fax: 505-646-6846

Email: plaumers@nmsu.edu

Resilt of blastx search of NCBI non-redundant protein database,
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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The information of this clone is available through the following
URL.
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/strain="DAOM 197198, Biosystematic Research Center,
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Tel: 81-559-81-6856
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Context: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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Location/Qualifiers
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                                                                        /dev_stage="stage 10.5"
/clone_ib="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
library"
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/clone lib="NIBB Mochii normalized Xenopus early gastrula
library"
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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The information of this clone is available through the following
URL.
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AGENCOURT 10304580 NICHD XGC Emb1 Xenopus laevis cDNA clone
IMAGE:5161647 5', mRNA sequence.
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Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTT 40
                                                                                                                                                                                                                                             2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTT 40
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                                                                                                                                                                          Score 23; DB 12;
Pred. No. 7.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="XL154a01"
/tissue_type="whole embryo"
                                                                   'tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
Xenopus laevis

    631
    organism="Xenopus laevis"

 organism * "Xenopus laevis"
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/db_xref="taxon:8355"
                  mol_type="mRNA"
db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://xenopus.nlbb.ac.jp.
Location/Qualifiers
                                                    /clone="XL210a01"
                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ096452.1 GI:17597377
                                                                                                                                                                          56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopodinae; Xenopus.
                                                                                                                                                                                                         29; Conservative
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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 29; Conserv
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Best Local Similarity
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CA791463
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KEYWORDS
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Xenopodinae, Xenopus,
Xenopodinae, Xenopus,
Is (Dases 1 to 832)

Is (Dases 1 to 832)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

In published (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Produment: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Baloscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Plane: LiAM11401 row: b column: 16
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo (stage 10)"
| Lab host="Dt1018 (plage-resistant)" |
| Lab host="Th1018 (plage-resistant)" |
| Clone lib="NICHD XGC Embl" |
| Anotes="Vector: pGWV-SFORT6; Site_1: NotI; Site_2: SalI; |
| Cloned unidirectionally. Primer: Olygo dT. Average insert size 1:55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
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S17 bp DNA linear GSS 16-DEC-1998
HS_3217_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3217 Col=19 Row=F, genomic survey
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1 (bases 1 to 517)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
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University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5161647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:8355"
CA791463
CA791463.1 GI:26038360
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                                                                                                                                                    RESULT 14
AZ896574/c
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JOURNAL
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AUTHORS
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Schistosoma japonicum
Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (Daess I to 542)
Hu, W. Yan, Q., Shen, D. K., Liu, F., Zhu, Z. D., Song, H. D., Xu, X. R.,
Wang, Z. J., Rong, Y. P., Zeng, L. C., Mu, J., Zhang, X., Wang, J. J.,
Xu, X. N., Wang, S. Y., Fu, G., Zhang, X. L., Wang, Z. Q., Brindley, P. J.,
McManus, D. P., Xu, C. L., Feng, Z., Chen, Z. and Han, Z. G.
Bvolutionary and biomedical implications of a Schistosoma japonicum
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Chinese National Human Genome Center at Shanghai
201203, P. R. China
1201: 86-21-50801919 (ex.45)
Pax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU722189 542 bp mRNA linear BST
SJMAEF03 SJM Schistosoma japonicum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%; Score 22.8; DB 28; Length 517; ilarity 79.4%; Pred. No. 8.2e+02; Conservative 0; Mismatches 7; Indels 0.
401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Fax: (207) Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Schistosoma japonicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="Plate=3217 Col=19 Row=F"
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/dev_stage="adult"
/lab_host="rabbits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                     High quality sequence stop: 517.
Location/Qualifiers
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/db_xref="taxon:6182"
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Location/Qualifiers
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VERSION
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SOURCE
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Gaps

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6 AACTACATAACAACCACCTTAGTCAGATACTACT 39

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Mus musculus (house mouse)

Kus musculus (house mouse)

Elkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Elkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

El (bases 1 to 725)

Sa Sao,S., Nierman, M., Malek,J., Shatsman,S., Akinret,B., Levins,M.,

Russell,D., Geer,K., Krol,M., Shvattsbeyn,A., Gebregeorgis,E.,

Russell,D., de Jong,P. and Fraser,C.M.

Russell,D., de Jong,P. and Fraser,C.M.

Other GSSE: RPCI-24-209C20.TJ

Contact: Shaying Zhao

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 bp mRNA linear EST 01-JUL-2000 BB224503 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530086005 3', mRNA sequence.
GSS 05-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.thgr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 209 row: C column: 20 Seq primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                           RPCI-24-209C20.TV RPCI-24 Mus musculus genomic clone RPCI-24-209C20, genomic survey sequence.
linear
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/clone="RPCI-24-209C20"
   725 bp
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                                                                                                                AZ896574.1 GI:13215519
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KEYWORDS
SOURCE
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Mus musculus

ORGANISM

REFERENCE

COMMENT

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Matches
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 328)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Itawa, M., Kadota, K., Kagawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, J., Kaiya, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsunyama, T., Maki, R., Mizuno, Y., Nakamura, M., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suamanra, T., Yamana, Y., Suzuki, H., Suzuki, H., Tagawa, A., Hayashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamanra, T., Yamanaka, I., Yano, R., Yasunishi, A., Hayashizaki, Y. Osshida, K., Yoshiki, A., Yoshino, M., Muramateu, M. and Hayashizaki, Y. Or Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-resegnsc.riken.go.jp,
URL:http://genome-resegnsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P. Nishiyama,Y., Westover,A., Itch,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Okazaki,Y. and Hayashizaki,Y. Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lib="RIKEN full-length enriched, adult male aorta
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/dev_stāge="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-45-503-9216
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source

FEATURES

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                                      0
55.1%; Score 22.6; DB 10; Length 328; 75.7%; Pred. No. 9.1e+02; ive 0; Mismatches 9; Indels 0;
                                                                                                                        110 AACTAACTATATACCAACCACCTAAGTGAGGTCTTAC 146
                                                                                  2 AATGAACTACATAACAACCACCTTAGTCAGATACTAC 38
                                         28; Conservative
Query Match
Best Local Similarity
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Search completed: March 25, 2004, 00:13:55 Job time : 2001.1 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
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Title: Perfect score: Sequence:	US-09-889-611A-60_COPY_2_42 41 1 gaatgaactacataacaaccccttagtcagatactacttt 41
Scoring table:	OLIGO_NUC Gapop_60.0 , Gapext 60.0
Searched:	3470272 seqs, 21671516995 residues
Word size :	0
Total number of	Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Listing first 45 summaries
Database :	GenEmb]:*

ge : GenEmbl:\*

1: 9b ba:\*
2: 9b\_htg:\*
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7: 9b\_pt:\*
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41: em\_htgo\_ouher:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AF234618 Homo gapi	51 Homo	1524	5917 Seque	356 Homo Bap	2543 Arabi	ACUZESSE HOMO BADI		oeduence	ALGEAGES OFFER SAL	Darting n	Rattus n	w	Seguen	Felis	AC022083 Homo sapi	Mous	Human DN	8888	339 Homc	Mus mus	73 Mouse	Lemur		Homo	Ношо	3674 Homo	5558 Homo	9347 Mus	9 Mus mus	5 Rattus	4 Zebrail	. Kattus	Ractus n	AIU/OSI/ DIOBODUII AF429950 Dlaemodiu	atatin A				0 0	ous prosopur	73417 Human DNA	AP000261 Homo sapi	F359360	
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di	Query e Match Length	7 90.2 4229	7 90.2 157284	7 90.2 189092	1 51.2 6182	46.3 3/490	46.3 /4330	9 46 3 220480	43 9 2000	43 9 143961	730051 6 67	43.9 215960	8 43.9 282132	7 41.5 1712	7 41.5 16918	7 41.5 107365	7 41.5 114149	7 41.5 117995	7 41.5 135455	7 41.5 148510	7 41.5 152560	7 41.5 157585	7 41.5 162215	7 41.5 162621	41.5 165764	7 41.5 173933	7 41.5 180905	7 41.5 188818	7 41.5 189715	7 41.5 205202	7 41.5 222932	7 41.5 231197	7 41.5 234545	7 41.5 269132	7727 7 7 7 7	39.0 1/66	6 39.0 4116	39.0 6160	39.0 6160	00000	1991 0 95 A	#TART 0 00 U	39.0 37650	6 39.0 51680	6 39.0 54488	
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RESULT 1 AF234618 LOCUS LOCUS ACCESSION VERSION VERSION SETMORDS SOUNCE ORGANISM		AF234618 4229 bp DNA linear PRI 29-MAR-2002	Homo mapiens megain gene, promoter region a	AF234618	AF234618.2 GI:19808130	Homo sapiens (human)	ORGANISM Homo sapiens
	RESULT 1 AF234618	,		<b>7</b>			ORGANISM H

ALIGNMENTS

VERSION AF234618.2 GI:19808130

KEYWORDS ...
SOURCE Home sapiens (human)
ORGANISM Home sapiens (human)
ORGANISM Home sapiens (contacts)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.
AUTHORS Miyata,T., Nangaku,M., Inagi,R. and Kurokawa,K.
TITLE Transcriptional regulation of a mesanglum-predominant gene, megsin JOURNAL Unpublished

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Direct Submission

Submisted (25-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA

Research, 320 Charles Street, Cambridge, NA 02141, USA

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Deawar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Levine, K., Liu, G., MacCan, C., MacGonald, P., Marquis, N., Matthews, C., MacGonald, P., Marquis, N., Matthews, C., Norman, C.H., O'Connor, T., O'Donnell, D., O'Mell, D., O'Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Redil, D., O'Law, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Redil, D., O'Love, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Stanger, J., Vassiliev, H., Viel, R., Travis, M., Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 18, 2001 this sequence version replaced gi:14277307.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                    Miyata,T., Nangaku,M., Inagi,R. and Kurokawa,K.
Direct Submission
Submitted (15-FEB-2000) Institute of Medical Sciences and
Department of Internal Medicine, Tokai University School of
Medicine, Bohseidai, Isehara, Kanagawa 259-1193, Japan
3 (bases 1 to 4229)
                                                                                                                                                                                                                                                                                                                      Submitted (29-MAR-2002) Institute of Medical Sciences and Department of Internal Medicine, Tokai University School of Medicine, Bohneidai, Isehara, Kanagawa 259-1193, Japan Sequence update by submitter Sequence Update his sequence version replaced gi:18000453.
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/db_xref="taxon:9606"
/chromosome="18"
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/product="megsin"
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6373 .16374
'note="1328 bp of bacterial transposon insertion in BAC
clone lib="RPCI-11 Human Male BAC"
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/rpt_family="LiM4c"
complement(25602. .25854)
/rpt_family="MIR"
26746. .26796
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/ rpt_family="MER81"
/ rpt_family="MER81"
/ rpt_family="MLT1U"
| 1396. 14009
/ rpt_family="AT_rich"
| 14011. 14115
/ rpt_family="(TA)n"
| complement [14942. 15044)
/ rpt_family="MIR3"
| 15156. 15298
| / rpt_family="L2"
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/rpt family="MSTA"
complement(24678. .25041)
/rpt family="MLT1A2"
25054. .25094
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complement(21559. .21386)
/rpt_family="MIR3"
22395. .22420
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complement (22788 . 22948)
/rpt_family="FRAM"
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complement(7416. .7621)
/rpt_family="MBR3"
complement(8163. .9090)
/rpt_family="L2"
                                                                                                                                                              /rpt_family="L1MC4a"
1834. .4338
                                                                                                                                                                                                                                          /rpt_family="LlMC4a"
complement(5742, .5899)
/rpt_family="MER5B"
6499, .6816
                                                                                                                                                                                                                         complement (4339. .5397) /rpt_family="LIMC4a"
       599. .635

/rpt_family="(T) n"

1040 .1077

/rpt_family="AT_rich"

1411. 1147

/rpt_family="LiP"

2632. .2992
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rpt_family="(TAAAA)n"
8332. .19566
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19567. .19587
/rpt_family="(CA)n"
19588. .20042
                                                                                                                                 3115. .3138
/rpt family="AT rich"
complement (3487. .382)
                                                                                          2632. .2992
/rpt_family="MLT1A1"
3115. .313a
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0043. .20064
                                                                                                                                                                                                              family="MLT1C"
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family="HAL1"
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3598. .9658
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/rpt_family="AT_rich"
27451. 27464
77pt_family="(CAAAA)n"
complement(28183. 28219)
/rpt_family="MR"
complement(28249. 28325)
/rpt_family="MIR"
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complement(29372. .29459)
/rpt_family="MIR"
29539. .30003
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complement(32019, .32103)
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31418. .31829
                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="MER66B"
30596. .30624
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AX346917.1 GI:18494803

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KEYWORDS
VERSION
                                           SOURCE
           Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 1, 2002 this sequence version replaced gi:11990731. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 2; Length 189092; 100.0%; Pred. No. 2.9e-12; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85659: contig of 85659 bp in length
85660 85759: gap of 100 bp
85760 163014: contig of 77255 bp in length
183015 163114: gap of 100 bp
163115 189092: contig of 25978 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-317G1"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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/db xref="taxon:9606"
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Manmalia; Editeria; Primates; Catarrini; Hominidae; Homo.

I (Dases I to 37490)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Binage, W., Blown, B., Brown, M., Bryant, N.P., Bubay, C.,

Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Caron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, M.L.,

Denn, A.L., Dingy, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,

Denn, A.L., Dingy, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,

Dugan-Rocha, S., Durbin, K.J. Earnhart, C., Edgar, D., Edwards, C.,

Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraquto, D.,

Flaggy, N., Fords, J., Barnhart, C., Gorell, J.H., Guevara, W.,

Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W.,

Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K.,

Hat, M., Hoyues, M., Holloway, C., Hollins, B., Homsi, F.,

Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L. E.,

Jacobson, B., Jaz, Y., Johnson, R., Montgomen, P., Martin, R.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Katovic, J., Li, J., Liz, Lichtarge, O., Lieu, C., Liu, J., Liu, R.,

Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R.,

Man, Maheshwari, M., Mapua, P., Marondel, I., Martin, R.,

Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M.,

Miner, Z., Mitchell, T., Mohabbat, R., Morlson, E., Nwokenkwo, S.,

Oguh, M., Okwuonu, G., Oragunye, N., Oriedo, R., Parce, A., Payton, B.,

Peery, J., Peers, L., Peters, L., Pickens, R., Perme, J., Peters, L., Puckes, R., Peters, L., Pickens, R., Peters, L., Pickens, R., Peters, L., Peters, L., Peters, L., Peters, L., Peters, R., Peters
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Homo sapiens 12 BAC RP11-81714 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="chemically treated genomic DNA (Homo mapienm)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 6; Length old.
Pred, No. 0.038;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
synthetic construct
artificial sequences.
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Gaps

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66563 GAATGAACTACATAACAACCACCTTAGTCAGATACTA 66599

1 GAATGAACTACATAACAACCACCTTAGTCAGATACTA 37

37; Conservative

Matches

linear

6182 bp

AX346917

RESULT 4 AX346917/c LOCUS

DEFINITION

ACCESSION

Seguence 1988 from Patent WO0200928. AX346917

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Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tanger, H., Tamerisa, A., Tamerisa, K., Tanger, H., Tannes, J., Tannes, J., Tanger, J., Tanger, J., Vanguez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., T., Zorrilla, S., Kuoherlapati, R., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-MRR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 37490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-SEP-2001) Human Genome Sequencing Center, Department
Submitted Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 37490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-0CT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 27, 2001 Lhis sequence version replaced gi:15145501.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                 (bases 1 to 37490)
                                                                                                                                                                                                                                                                                                                                                                                                  Submission
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AUTHORS
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse Bequences.

Genes and Region of Sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low Coverage. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

Location/Qualifiers QUALSTAT-REPORT.

/organism="Homo sapiens" /mol\_type="genomic\_DNA" /db\_xref="taxon:9606"

/chromosome="12"

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FEATURES
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repeat_region
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http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
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note="overlaps bases 5470. .7000 of clone AC087316"
                                                                                                                                                                                                                                                                                                                                                                                      /function="polymorphic site"
8251. .8561
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                                           function="clone overlap'
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complement (3002. .3250)
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complement (3285. .3576)
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634_.9724
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complement(8980. .9253)
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                                                                                                                                /rpt_family="Alusg"
complement (3580. .3878)
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complement (3986. .4297)
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12127, .12191
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complement(5007...530
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/rpt_family="AT_rich"
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rpt family="MER102"
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8674. .8802
/rpt_family="MER33"
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complement (9333, .96
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4321. .4351
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1877. .6956
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3843. .8979
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8844. .8979
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13263. 13386
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/rpt_family="{C
16938. .17092
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standard_name
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VVVENREEEQLTAWPSPEAANSLIDNFYSLTDHERTWKAVDPESYVQTVIEKIEKKRA
DTRKVITEFEWDELMPOVONSELADLSPTEADKLIPYADKKUMLSKRAMGSTGVDAL
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LRKRVVGNPOFKFLSTINNSRFSFYNGLVIAYSRVLMPSKMLSKSDDCTATVDGFLS
CLOLEKRESGYDIDMIDLIDCFARLEDADYSANVPOPOHLSCYMQPPHTPETSPFLP
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DFLVAHSQVLPGYTPPGSYLLKMKMLDAKKKELTCIKFSFDIGLRASVADI"
complement (2599. .3192)
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YGYRCQRELTTRVVESPLFEPIKPTDSRNSFYTSI ILGYGYGUAPSQKLKTKSEVFDG

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IDTIKLTAQVPVCBPUNDHAKEVFSPRANGINDIRAPAPKSTDSKCSFYLRLVDGYSRVLRR

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APIEPPPEIRSCVERTYLLIPVSKOGLEIERKOMBLSANDDARHRVWSTDPYHAFYQLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYCTRSHISASPTTTPRTRRRQRESNGTLPPGQERFDFEDDESDTVVVEVLGLTEEVI
KGFPKLPYEEARVSYSLQKESSTTSCCSICLADYKKMDMIRVLPDCNHLFHDNCVDPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MNATVVPPYSGHWLINTDRMGGLAYGIGVSIGILMLITTITLTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MARKKVRAAWIRDDRMRRASLKRRLTGLIKKVNELSILCDMRAS/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1047. .7775
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  complement (join (822. .929, 1126. .1286, 1468. .1569,
                                1744. .1834))
/note="contains similarity to unknown protein
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Mistamura, 1.

Direct Submission

Submitted (22-JUN-2000) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0932, Japan (B-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaosekazusa.or.jp
Address for correspondence: kaosekazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi.bin/agd_graph.cgi?c=F15M7
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
RetGenes (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NecGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlini.zool.lastate.edu/cgi-bin/sp.an-SE/)
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://gremme.wustl.edu/eddy/tRNAscan-SE/)
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is MHRIS and the 3' clone is NPHIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP002543 74350 bp DNA linear PLN 27-DEC-2000 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F15M7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katoh, T., Asamizu, E., Sato, S., Nakamura, Y., Kotani, H.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Unpublished
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                                                                                                                                                                                                                                                                                                                                          0.53;
complement (18236. 18539)
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complement (18545. 18671)
/rpt_family="FLAM_C"
19365. 19386
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                              family="Alu"
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                                                                                                                                                                                                                                                                                                                                          Pred. No.
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                                                                                                                                                                                                                                    19618. .19920
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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19618.
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     repeat_region
                                                             repeat_region
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VERSION
KEYWORDS
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JOURNAL
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pieces
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Best Local $
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REFERENCE
AUTHORS
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JOURNAL
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AUTHORS
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AC026558
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KEYWORDS
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VTGSKKWVLFPPDVVPPGVHPSPDGABYACPVSIIEWFWNFYDDTKDWBKKFIECI
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COMplement (job.1 (28281. 28383, 28556. 28602, 28740. 30146))
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EGGLLDGMPALEKWSRDYLTKVVGDVEFAVGPVEMKLEKYFRYSDF
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LMLHDIARAGKTVITTIHQPSSRLFHRFDKLILLGRGSLLYFGKSSEALDYFSSIGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="contains similarity to unknown protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (join (32678. .32984,34934. .35616))
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similar to unknown protein"
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CDS

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Homo sapiens clone RP11-637N6, WORKING DRAFT SEQUENCE, 23 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   Score 19; DB 8; Length 74350;
Pred. No. 0.49;
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------- Project Information
Center project name: L7470
Center clone name: 637, N 6
                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                  46.3%; Sco...
100.0%; Pred. No. v.
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AC026558.3 GI:8077003
HTG: HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. In the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                        Insert size: 154194; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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1.156394
Organism="Homo sapiens"
| mol_type="genomic DNA"
| db_xref="texon:9606"
| clone="RP1-637N6"
| clone="lib="RPCI-11 Human Male BAC"
  Insert size: 163000; agarose-fp

    1014
    note="assembly_fragment"

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AC023973 22-6EP-2000 Homo sapiens chromosome 12 clone RP11-793A9 map 12, WORKING DRAFT SEQUENCE, 28 unordered pieces.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 12, clone RPI1-793A9
Unpublished
2 (bases 1 to 220480)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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vector_side:right"
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Matches 19; Conservative
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JOURNAL

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gap of 100 bp
contig of 17765 bp in length
gap of 100 bp
contig of 13834 bp in length
gap of 100 bp
gap of 101 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5: contig of 100 bp
5: contig of 11244 bp in length
7: gap of 100 bp
6: contig of 1272
                                                                                        gap of 100 bp
contig of 6381 bp in length
gap of 100 bp
contig of 5395 bp in length
gap of 100 bp
gap of 6317 bp in length
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contig of 14916 bp in length
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                                                                          contig of 6025 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                   100 bp
of 8300 bp in length
                                                                                                                                                                                                                                                                                                        gap of 100 bp
contig of 9098 bp in length
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contig of 6834 bp in length
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1. .2203
inote="assembly_fragment"
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/note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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8424. .22156
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6778. .32091
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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gap of
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2304. 3531
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Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreitza, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Hotton, L., Karatas, A., Klein, J., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McCwan, F., McGurk, A., McKernan, K., Lehoczky, J., Levine, R., McGurk, A., McKernan, K., McHeeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Direct Submission

Al Submitted (20-FeB-2000) Whitehead Institute/MIT Center for Genome Neset Mere identified using RepeatMasker:

All repeats were identified using RepeatMasker:

All tepeats were identified using RepeatMasker:
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 234000; agarose-fp
Insert size: 217780; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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gap of 100 bp
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of 1425 bp in length
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of 3483 bp in length
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of 4421 bp in length
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Submitted (30-OCT-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan 2-1-2, Tsukuba, Ibaraki 305-8602, Japan 11:tsasaski@mias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel.81-298-38-7441, Faxs1-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed are based on estimates that have provided by the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence.
                                                                                                                 AP005862 143961 bp DNA linear HTG 31-OCT-2002 Oryza sativa (japonica cultivar-group) chromosome 9 clone OSJNBa0038K02, *** SEQUENCING IN PROGRESS ***.
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                                                                                                                                                                                                              AP005862.1 GI:24430392
HTG; HTGS PHASE2.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 159056)
                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
clone:OSJNBa0038K02
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2 (bases 1 to 143961)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
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Location/Qualifiers
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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tive 0; Mismatches
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Sequence 5681 from Patent W003000898.
AX655811
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148950. .161417
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                                                                                                                                                                            Direct Submission
Submitted (20-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 4, 2003 this sequence version replaced gi:28372080.
Center: Genoscope / Centre National de Sequencage
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Upstream BAC (overlapping the T7 end) : OSJNBa0021D06 (AC=BX000560)
Downstream BAC (overlapping the SP6 end) : OJ1618_C05 (AC=AL713952)
Downstream BAC (overlapping the SP6 end) : OJ1618_C05 (AC=AL713952)
FINISHED SEGMENT STARTS AT BASE 5389
FINISHED SEGMENT ENDS AT BASE 159056
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Segurens, B., Pelletiez, E., Scarpelli, C., Salanoubat, M., Weissenbach, J. and Quetier, F.
Oryza sativa chromosome 12 sequencing
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
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Contact: SeqRef@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="12"
/clone="OSJNBb0071117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   Center code: GS
                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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  AUTHORS
                                                                             TITLE
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Gunzatne, D., Gablei, A., Gattle, R., Hanland, R
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15 Marzy, D. Marzie, Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allan, H., Alsbrooks, S., Adin, A., Augulano, D., Allan, C., Allan, H., Alsbrooks, S., Adin, A., Baranted, M., Benahmed, F., Balden, M., Allan, M., Balak, B., Baranted, M., Barnstead, M., Baranted, M., Barante, D., Chen, Z., Chu, J., Chang, C., Butch, P., Burral, M., Carter, M., Cavazou, C., Dieg, M., Carter, M., Cavazou, C., Dieg, M., Carter, M., Carter, M., Cavazou, C., Dieg, M., Chang, C., Chen, Z., Chu, J., Chang, S., Dunn, A., Duchin, M., Duya, K., Davis, C., Davy, Carroll, L., Cart, M., Carter, M., Sugan, A., Barante, M., Carter, M., Guevara, M., Duyla, Roche, S., Dunn, M., Dutya, K., Duran, M., Dugan, Roche, S., Dunn, M., Dutya, M., Carter, M., Guevara, M., Gunzara, M., Marla, M., Marla, M., Haviak, P., Haviak, P., Hawes, A., Hunk, S., Mani, C., Hamilton, C., Hariak, P., Mares, J., Hunk, S., Margathy, S., Kally, S., Margathy, M., Lavan, M., Martin, K., Martin, M., Martin, S., Martin, K., Martin, S., Sabaternak, S., Paul, M., Storay, G., Selar, M., Savart, G., Spart, M., Storay, C., Shart, M., 
                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus clone CH230-177G10, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                   43.9%; Score 18; DB 2; Length 215960; 100.0%; Pred. No. 1.8;
                                                                                   0; Indels
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                       100.0%; Pred. ...
                                                                                                                                                                                                       91069 AATGAACTACATAACAAC 91086
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                Query Match
Best Local Similarity 100.(
Matches 18; Conservative
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                         31293: contig of 31293 bp in length 42669: contig of 11276 bp in length 42769: gap of unknown length 42769: gap of unknown length 55798: contig of 13029 bp in length 62523: contig of 625 bp in length 62523: contig of 6625 bp in length 80112: gap of unknown length 10120: contig of 17349 bp in length 91361: contig of 17349 bp in length 91361: contig of 17349 bp in length 171226: contig of 79765 bp in length 171226: contig of 1253 bp in length 18352: contig of 1253 bp in length 185305: contig of 1253 bp in length 185305: contig of 1253 bp in length 185405: contig of 1140 bp in length 186545: contig of 1140 bp in length 186545: contig of 1140 bp in length 187946: gap of unknown length 189065: contig of 1119 bp in length 189065: contig of 1119 bp in length 189065: contig of 1831 bp in length 190863: gap of unknown length
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contig of 2626 bp in length
gap of unknown length
contig of 1454 bp in length
gap of unknown length
contig of 2060 bp in length
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/organism="Rattus norvegicus"
/organism="Resonic DNA"
/db_xref="taxon:10116"
/clone="Reson:1059"
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55899. .57107
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80113. .82141
/note="wgs_contig"
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TITLE

COMMENT

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Oryza sativa (japonica cultivar-group) cDNA clone:J033003A15, full insert sequence.
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FLI_CDNA, CAP trapper.
Oryza estiva (japonica cultivar-group)
Oryza estiva (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
211185: 345. --
212868: contig of 1703 bp in length
212868: gap of unknown length
216482: contig of 3514 bp in length
3 216582: gap of unknown length
3 218704: gap of unknown length
15 218704: gap of unknown length
15 218705: contig of 3061 bp in length
16 221865: gap of unknown length
17 225831: contig of 3061 bp in length
18 225831: contig of 3061 bp in length
18 225931: gap of unknown length
18 233231: gap of unknown length
18 244973: contig of 17200 bp in length
19 246570: contig of 11742 bp in length
17 246570: contig of 11742 bp in length
17 246570: contig of 1877 bp in length
18 25770: gap of unknown length
18 275653: contig of 6072 bp in length
18 275653: contig of 6572 bp in length
18 275653: contig of 6379 bp in length
18 275653: contig of 6379 bp in length
18 275653: contig of 6379 bp in length
18 27563: contig of 6379 bp in length.
18 282132: contig of 6379 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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43744. .45689
/note="wge contig"
64402. .68669
/note="wge contig"
79411. .83544
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L13702. .115613
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15664. .116916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="wgg_contig"
.91871. .193903
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L05471, .106633
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107196. .108531
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08632. .110536
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Matches 18; Conservative
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AK073122/c
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                                                                                                                                                                                                                           Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Flaza, Housen, TX 77030, USB of Medicine, One Baylor Flaza, Housen, TX 77030, USB of Medicine, One Sep 26, 2002 this sequence version replaced gi:21738290.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (Attp://www.hggc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_daraft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                    Submitted (09-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3. (bases I to 282132)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH230-177G10

------- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 212218 bases at least Q40

Consensus quality: 222117 bases at least Q30

Consensus quality: 222410 bases at least Q30

Consensus quality: 226410 bases at least Q30

Consinuered insert size: 2503059; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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gap of unknown length
contig of 12426 bp in length
gap of unknown length
contig of 1224 bp in length
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gap of unknown length
contig of 29591 bp in length
gap of unknown length
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unknown length
of 1544 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
Center code: BCM
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               2 (bases 1 to 282132)
Worley, K.C.
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Query Match
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                                                           The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Dishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iuja,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Ishibiki,J., Masudo,K., Yokomizo,S., Niikura,J., Narikawa,R., Sugiyama,A., Mauno,K., Yokomizo,S., Niikura,J., Kusumegi,T., Oka,M., Rawamata,M., Yoshimura,A., Mikura,J., Kawai,J., Carninci,P., Adachi,J., Alzawa,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Alzawa,K., Rikini,Y., Itch,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sato,R., Shibata,K., Shibata,A., Shiraki,T., Sohino,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayastu, N., Hiramoto, K., Hiraoka, T., Imayashida, Y., Ishakawa, M., Inamura, K., Imanura, K., Ishikawa, M., Itoh, M., Kagawa, T., Kanagawa, S., Katoh, H., Yawagashira, N., Kawai, T., Kawamata, M., Kikuchi, S., Kishikawa, Hirozane, T., Kishimoto, N., Kobayashi, M., Koya, S., Kurihara, C., Kurosaki, T., Kusunegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003)
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Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Fujimura, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y.; Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Niikura, J., Nishi, K., Nomura, K., Nomura, K., Numasaki, R., Ohneda, E., Ohne, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suyani, R., Suzuki, K., Suyami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, K., Xie, Q., Yahagi, W., Yamanoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail-skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, N., Hiramoto, K., Hiraoka, T., Hori, F., Ilmanura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, L., Kanagawa, S., Katoh, H., Kawal, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Ehrhartoideae; Oryzeae; Oryza.
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JOURNAL
                                      REFERENCE
                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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COMMENT

TITLE

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Koya,S., Kurihara,C., Matenyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Osato,M., Saitoh,H., Sakai,C., Sakai,K., Sakaume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="unassigned DNA"
/mol type="taxon:32630"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                    organism="Oryza sativa (japonica cultivar-group)"
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1590 03-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 1712;
13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1590 from Patent W00200928.
AX346519
                                                                                                                                                                                                                                                                                                                                                                                 41.5%; Score 17; DB 100.0%; Pred. No. 13; iive 0; Mismatches
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                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                 /db xref="taxon:39947"
/clone="J033003A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: March 25, 2004, 02:32:49 Job time : 1708 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 ACCACCTTAGTCAGATA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial sequences.
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synthetic construct
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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nucleic search, using sw model OM nucleic

March 25, 2004, 00:14:02 ; Search time 249 Seconds Run on:

(without alignments)
699.502 Million cell updates/sec

US-09-889-611A-60\_COPY\_2\_42 Title:

1 gaatgaactacataacaacc..........ccttagtcagatactacttt 41 Perfect score: Sequence:

Gapop\_60.0 , Gapext 60.0 OLIGO NUC Scoring table:

3373863 segs, 2124099041 residues Word size : Searched:

Total number of hits satisfying chosen parameters:

6747726

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

N\_Geneseq\_29Jan04:\* Database :

genesequ1988s; genesequ2000s; genesequ2001as; genesequ2001as; genesequ2001as; genesequ2003as; genesequ2003as; genesequ2003as;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

## SUMMARIES

Description		Aaa71434 Human meg	Aaa71449 Human meg	Aaa71448 Human meg	Aaa71453 Human meg	Aaa71452 Human meg	Abl34015 Human imm		Ada72356 Rice gene		Adb16926 Human DYX		Abl07442 Drosophil	Abk31272 Signal tr	Abl70233 Chemicall	Aad46721 Human tra	Aac13384 Human sec	Aah71525 Human cer	Aca44540 Prokaryot	Acf72327 Staphyloc	Aat13163 SCSV segm	Aas89552 DNA encod	Aas87858 DNA encod
đ	AAA71435	AAA71434	AAA71449	AAA71448	AAA71453	AAA71452	ABL34015	AAC39949	ADA72356	ABL33617	ADB16926	ABL07443	ABL07442	ABK31272	ABL70233	AAD46721	AAC13384	AAH71525	ACA44540	ACF72327	AAT13163	AAS89552	AAS87858
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Length	1431	128	30	30	25	23	6182	1523	2000	16918	50000	1652	3991	6160	6160	17993	241	756	789	951	1002	1188	1189
% Query Match	100.0	91.6	73.2	73.2	61.0	56.1	51.2	46.3	43.9	41.5	41.5	39.0	39.0	39.0	39.0	39.0	36.6	36.6	36.6	36.6	36.6	36.6	36.6
Score	41	40	30	30	25	23	21	19	18	17	17	16	16	16	16	16	15	15	15	15	15	15	15
Result No.		73	٣	4	Ŋ	v	0 7	ထ ပ	Q	C 10	11	12	c 13	c 14	c 15	c 16	c 17	18	19	20	c 21	22	23

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Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 41; Conservative 0; Mismatches 0; Indels C

Sequence 1431 BP; 466 A; 266 C; 303 G; 394 T; 0 U; 2 Other;

Aas89553 DNA encod	Aas53391 Haemophil	Aca34260 Prokaryot	Aah73359 Human cer	Abv25202 Human pro	Abv24391 Human pro	Aac69532 Human sec	Ada55988 Gene enco	Ada39801 Human sec	Acc50434 Human sec		Aaq97797 Clone pTd	Abl10239 Drosophil	Adb63696 Human cDN	Abl33653 Human imm	Ab132228 Human imm	Aas59391 Mouse cDN	Aag59389 Mouse cDN	Aas59390 Mouse cDN		Abk31306 Signal tr	Abl70281 Chemicall
AAS89553	AAS53391	ACA34260	AAH73359	ABV25202	ABV24391	AAC69532	ADA55988	ADA39801	ACC50434	ABI99599	AAQ97797	ABL10239	ADB63696	ABL33653	ABL32228	AAS59391	AAS59389	AAS59390	ABL33216	ABK31306	ABL70281
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1254	1617	1617	1698	1698	1698	1886	1886	1886	1886	1966	1986	2084	2560	5926	6049	6052	6075	6120	6191	6191	6191
36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6
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## ALIGNMENTS

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This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (I) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating protein s (sepecially transcription factors). This sequence represents a fragment of the human megsin promoter which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                DNA for promoter region of megsin useful for screening proteins
                                                                                                                                     Promoter; megsin; human; protein isolation; screening. ss.
                                                                                                            Human megsin promoter fragment DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 45pp; Japanese.
                           AAA71435 standard; DNA; 1431 BP
                                                                                                                                                                                                                                                                           99JP-00015667.
                                                                                                                                                                                                                                                25-JAN-2000; 2000WO-JP000350.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-543257/49.
                                                                                                                                                                                                                                                                                                     (KURO/) KUROKAWA K.
(MIYA/) MIYATA T.
                                                                                                                                                                                           WO200043528-A1.
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                          25-JAN-1999;
                                                                                 01-DEC-2000
                                                                                                                                                                                                                     27-JUL-2000.
                                                                                                                                                                                                                                                                                                                                              Miyata T;
                                                       AAA71435;
RESULT 1
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AAA71434

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This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating protein (sepecially transcription factors).

AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 73.2%; Score 30; DB 3; Length 30; Local Similarity 100.0%; Pred. No. 2.5e-07; les 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 BP; 12 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human megsin promoter PCR primer SEQ ID NO: 15.
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                                                                                                                                                                                                                                                                                              Example 5; Page 40; 45pp; Japanese.
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                                                                                       99JP-00015667.
                                                  25-JAN-2000; 2000WO-JP000350
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                                                                                                                                                                                                                      WPI; 2000-543257/49.
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                                                                                                                            KURO/) KUROKAWA K.
                                                                                                                                                (MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIYA/) MIYATA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200043528-A1
                                                                                       25-JAN-1999;
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                 27-JUL-2000.
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                                                                                                                                                                                   Miyata T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA for promoter region of megsin useful for screening proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.6%; Score 40; DB 3; Length 128; 100.0%; Pred. No. 5.2e-13; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          Promoter; megsin; human; protein isolation; screening. ss.
                                       1303 GAATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 128 BP; 44 A; 29 C; 24 G; 29 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AATGAACTACATAACAACCACCTTAGTCAGATACTACTTT 41
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                                                                                                                                                                                                                                                         Human megsin promoter fragment DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 32; 45pp; Japanese.
                                                                                                                                                AAA71434 standard; DNA; 128 BP.
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Best Local Similarity 100...
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                                                                                                                                                                                 AAA71434;
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This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the

WO200043528-A1

Homo sapiens.

RESULT 3 AAA71449

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Gape

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Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
                                                    Human megsin promoter PCR primer SEQ ID NO: 19.
                                                                                                                                                                                                                                  25-JAN-2000; 2000WO-JP000350.
                                                                                                                                                                                                                                                                    99JP-00015667,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL34015 standard; DNA; 6182
                    01-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-543257/49
                                                                                                                                                                                                                                                                                                       (KURO/) KUROKAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                          MIYA/) MIYATA T.
                                                                                                                                                             WO200043528-A1
                                                                                                                                                                                                                                                                    25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                           Ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002.
                                                                                                                                                                                              27-JUL-2000
                                                                                                                                                                                                                                                                                                                                                             Miyata T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL34015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel DNA sequence (1) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (1); (2) a cell transformed by the above vector; and (3) protein produced using (1). (1) as useful for screening and isolating proteins (especially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
above vector; and (3) protein produced using (1). (1) is useful for screening and isolating proteins (especially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter; megsin; human; protein isolation; screening. PCR primer; ss.
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                                                                                                                       73.2%; Score 30; DB 3; Length 30; 100.0%; Pred. No. 2.5e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%; Score 25; DB 3; Length 25; 100.0%; Pred. No. 0.00017; ive 0; Mismatches 0; Indels
                                                                                       Sequence 30 BP; 13 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 8 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human megsin promoter PCR primer SEQ ID NO: 20.
                                                                                                                                                                                                2 AATGAACTACATAACAACCACCTTAGTCAG 31
                                                                                                                                                                                                                                  1 AATGAACTACATAACAACCACCTTAGTCAG 30
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                             30; Conservative
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                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KURO/) KUROKAWA K.
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                                                        invention
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AAA71452
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                                                                                                 This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (I) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (especially transcription factors). AAA71434-A71469 represent PCR primers used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation; antiasthmatic; antiartariosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulant; ophthalmological; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anamatory; cancer; eye disease; arteriosclerosis; and permit inflammatory. Allo, antidiabetic disease; Allo, epilepsy; neurofibromatosis; harmatodia arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
DNA for promoter region of megain useful for screening proteins
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                                                                                                                                                                                                                                                                                                                                                                         56.1%; Score 23; DB 3; Length 23; 100.0%; Pred. No. 0.0023; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 1988.
                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 11 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAATGAACTACATAACAACCACC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAATGAACTACATAACAACCACC 23
                                                    Example 4; Page 42; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP007537.
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9905-0132466P

9905-0132467P

9905-0134218P

9905-0134218P

9905-0134218P

9905-0134218P

9905-0134218P

9905-0134218P

9905-013470P

9905-0134724P

9905-0134724P

9905-0135224P

9905-0135224P

9905-0135228P

9905-0135228P

9905-0135228P

9905-0135228P

9905-0135228P

9905-0135228P

9905-0135228P

9905-0137224P

9905-0137228P

9905-0137228P

9905-0138647P

9905-0139458P

9905-0140353P
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99US-0142055P.
99US-0142390P.
99US-0142803P.
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99US-0142977P.
99US-0143542P.
99US-0143624P.
99US-0144005P.
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99US-0144086P.
99US-0144325P.
99US-0144331P.
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990S-0144334P.
990S-0144335P.
990S-0144352P.
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99US-0144884P.
99US-0144814P.
30 - APR - 1999 ; 

30 - ARR - 1999 ; 

65 - MAX - 1999 ; 

66 - MAX - 1999 ; 

67 - MAX - 1999 ; 

11 - MAX - 1999 ; 

14 - MAX - 1999 ; 

14 - MAX - 1999 ; 

15 - MAX - 1999 ; 

16 - MAX - 1999 ; 

17 - MAX - 1999 ; 

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19 - MAX - 1999 ; 

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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disporders, including eye diseases such as retinopathy, neovascular glaucoma an macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6182 BP; 1934 A; 37 C; 1059 G; 3152 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Match 51.2%; Score 21; DB 6; Length 6182; Local Similarity 100.0%; Pred. No. 0.029; les 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1988; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 26493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1306 AACTACATAACAACCACCTTA 1286
                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AACTACATAACAACCACCTTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC39949 standard; DNA; 1523 BP
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99US-0123180P.
99US-0125784P.
99US-0126264P.
99US-0126264P.
99US-012624P.
99US-0128234P.
99US-0128234P.
99US-0138210P.
99US-0130510P.
99US-0130510P.
                30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
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                                                                                         Olek A, Piepenbrock C,
                                                            (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                      WPI; 2002-130909/17
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23-APR-1999;
23-APR-1999;
28-APR-1999;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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                                                                                                                                                                                    methylation.
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19-APR-1999;
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9905-0145088P

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9905-014518P

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9905-014518P

9905-0145218P

9905-0147303P

9905-0147303P

9905-0147303P

9905-0147303P

9905-0147303P

9905-014932P

9905-014932P

9905-014932P

9905-014932P

9905-014932P

9905-015565P

9905-015958P
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28-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
08-OCT-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
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23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
27-JUL-1999;
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28-UUL-1999,
02-AUG-1999,
02-AUG-1999,
04-AUG-1999,
04-AUG-1999,
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25-AUG-1999;
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27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
         21-JUL-1999;
22-JUL-1999;
22-JUL-1999;
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22-JUL-1999;
23-JUL-1999;
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15-SEP-1999;
16-SEP-1999;
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22-SEP-1999;
23-SEP-1999;
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10-AUG-1999;
11-AUG-1999;
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13-AUG-1999;
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20-AUG-1999;
23-AUG-1999;
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17-AUG-1999
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20-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response to a plant ting plant
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting gene expression.
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E Z, Zhu T, Zou G;
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                                                                                                                                                                                                                                          46.3%; Score 19; DB 3; Length 1523; 100.0%; Pred. No. 0.4; 0; Mismatches 0; Indels
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Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 5681; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                      646 CAACCACCTTAGTCAGATA 628
                                                                                                                                                                                                                                                                                         16 CAACCACCTTAGTCAGATA 34
                                                                                                                                                                                                                                                                                                                                                                         ADA72356 standard; DNA; 2000 BP
99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160814P.
99US-01608118P.
99US-0160811P.
99US-0160811P.
99US-0161981P.
99US-0161404P.
99US-0161406P.
99US-0161406P.
99US-016131P.
99US-016131P.
99US-016131P.
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001WO-IB001105.
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                                                                                                                                                                                                                                                                  19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice gene, SEQ ID 5681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chang H, Chen W, Co
Katagiri F, Quan S,
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                                                                                                                                                                                                                                                     Similarity
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 21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic; antiarthritic; antidiabetic; antipporiatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
useful for conferring resistance to resistance or tolerance to a plant bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16918 BP; 4516 A; 235 C; 3886 G; 8281 T; 0 U; 0 Other;
                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulgant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.5%; Score 17; DB 6; Length 16918; 100.0%; Pred. No. 5.2; ative 0; Mismatches 0; Indels (
                                                                                                         Query Match 43.9%; Score 18; DB 7; Length 2000; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                        Sequence 2000 BP; 576 A; 406 C; 423 G; 593 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1590; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 1590.
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                                                                                                             43.5°,
100.0%; Pre-
0; M
                                                                                                                                                                                                                                                                                                               ABL33617 standard; DNA; 16918 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                       9 TACATAACAACCACCTTA
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                      illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Local Si..
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                                                                                                                                                                                                                                                                                RESULT 10
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This invention relates to a novel isolated human gene DXXC1 that is functionally related to dyslexia, more particularly it describes single muclecited polymorphisms thought to predispose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DYXC1 has been isolated to chromosome 15q21), which manifests itself as a specific reading disability. Specifically, DYXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DYXC1 gene, and also provides DYXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide is the partial genomic sequence of the human DYXC1 chromosomal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                  ds; human; DYXC1; dyslexia; neurological disorder; chromosome 15q21; reading disability; phonological processing; rapid naming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50000 BP; 15686 A; 9567 C; 10158 G; 14589 T; 0 U; 0 Other;
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                                                                                                                                                                                                                  Human DYXC1 DNA, chromosomal gene region nucleotides 1-50000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.5%; Score 17; DB 8; Length 50000; 100.0%; Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taipale M, Nopola-Hemmi J, Kaminen N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 5.1 iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; Page 55-69; 135pp; English.
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                                                                                                         ADB16926 standard; DNA; 50000 BP
6093 ACTACATAACAACCACC 6077
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Best Local Similarity 100.0
Watches 17, Conservative
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                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                         verbal short-term memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LICH ) LICENTIA LTD
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                                                                                                                                                                                                                                                                                                                                                             WO2003068814-A1.
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                              ADB16926;
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                                                                         RESULT 11
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7 ACTACATAACAACCACC 23

Conservative

Matches

Similarity

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 16808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila, developmental biology; cell signalling; insecticide;
             Drosophila melanogaster expressed polynucleotide SEQ ID NO 16811
                                         Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1652 BP; 434 A; 391 C; 406 G; 421 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 16811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL07442 standard; cDNA; 3991 BP.
                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 CAÁCCACCTTÁGTCAG 592
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                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                    23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Matches 16; Conservative
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                                                             pharmaceutical; gene; ss
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                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75
                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY
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                                                                                                                          WO200171042-A2.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1815-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3991 BP; 1159 A; 901 C; 865 G; 1066 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
39.0%; Score 16; DB 4; Length 3991;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                     Claim 1, SEQ ID NO 16808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal transduction associated gene modified DNA #58.
                                                                                     Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK31272 standard; DNA; 6160 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2143 CAACCACCTTAGTCAG 2128
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23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                     Adame M,
                                                                                                                       WPI; 2001-656860/75
                                                   (PEKE ) PE CORP NY
                                                                                                                                         P-PSDB; ABB63339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200926-A2
                                                                                                                                                                                                         interactions.
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Synthetic.
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                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK31272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite.

Malo disclosed are oligomucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the disponsis and/or therapy of genetic and epigenetic parameters of obtained from calls or cellular components which contain DNA, e.g. cellular sequence embedded in paraffin such a stsue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the disponsis and therapy of diseases associated with signal transduction or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                      Claim 1; SEQ ID NO 115; 24pp; English.
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ó Gaps ö Sequence 6160 BP; 1580 A; 139 C; 1637 G; 2804 T; 0 U; 0 Other; 39.0%; Score 16; DB 6; Length 6160; 100.0%; Pred. No. 20; 0; Indels 0; Mismatches 7 ACTACATAACAACCAC 22 Local Similarity 100. Query Match Matches ð

Search completed: March 25, 2004, 02:04:13

: 252 secs

Job time

68 ACTACATAACAACCAC 53

Cell signalling, cytosine methylation, cell signalling disease; cancer; tumour; cytostatic; ds. ABL70233 standard; DNA; 6160 BP (first entry) 01-JUL-2002 ABL70233; RESULT 15 

Chemically treated cell signalling DNA sequence#62.

Unidentified.

WO200202807-A2.

10-JAN-2002

29-JUN-2001; 2001WO-EP007471.

30-JUN-2000; 2000DE-01032529, 01-SEP-2000; 2000DE-01043826.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2002-154758/20.

Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.

Claim 1; SEQ ID NO 123; 24pp + Sequence Listing; English.

The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the

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invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  39.0%; Score 16; DB 6; Length 6160; 100.0%; Pred. No. 20; tive 0; Mismatches 0; Indels
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AI188862 qd27a12.x
AL189827 Tetraodon
CF608248 GEMMA01_0
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609.129 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                    27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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549 9 AI188862
931 29 CNS02BGQ
72 14 CF608248
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                                                  - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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	13	17	Н	695	13	BQ874693	щ		QGI6A13.y
O	14	11	Н	782	29	CG114080	J		PUJGG81TD
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υ	21	16	Φ	259	10	BF067189	щ	3F067189	st34a12.y
	22	16	σ	300	σ	AV169199	A	7169199	AV169199
	23	16	σ.	381	10	BF373680	ш,	3F373680	MR3-SN001
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	34	16	σ	486	14	CF373282		CF373282	CSECS085G
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υ	42	16	Φ	564	10	BE347205	щ	3E347205	8p36c03.y
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υ	44	16	σ,	574	12	BI701328	ш (	31701328	Bag57e03.
	45	16	σn .	576	14	CD799091		18066702	EST 12/52
						ALIGNMENTS			
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RES	RESULI 1								
101	Since	BF	5378			294 bp	mRNA linea		EST 24-NOV-2000
DEF	DEFINITION	ò	-NT0028-	-080700-28	-28	6-c08 NT0028 Ho	NT0028 Homo sapiens cDNA,		sequence.
ACC	ACCESSION	BF36	5378						
VER	VERSION	BF365	5378.1	GI	:11327	403			
KEY	KEYWORDS	EST.	, to	(remind) or	1				
Ö	ORGANISM	Homo	sapi	nn 90	1001				
į		Euka	ryota;	Metazo	)a;	~	Craniata, Vertebrata,	щ	leostomi;
i		Mamm,		Eutheria;			rhini; Hominic	dae; Homo	ċ
REF.	REFERENCE	٦ <u>۲</u>	(Dages		9,5		Verjovski-Almeida.S	ď	iones.M.R.
¢	CALLEGA	Naga	Nagai, M.A.		lva	. ผ	ιщ	ë	:
		Gold	Goldman, G.		val	ho, A.F., Matsuk	., Bai	S	mpson, D.H.,
		Brun	Brunstein, A.,	A., dec	711V	a, P.S., B	, Jong	97	יים איני ביים די מי שני
		Sino	Simpson.A.J.	., soan	20	r., bremcami, r.	מדם ב	y S	
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Σc	MEDLINE	2020	20202663	. Acad	n n	. 0.5.A. 97	0645-7646 /	(0007)	
	PUBMED	1073	7800						

Contact: Simpson A.J.G. Liaboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

10737800

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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                  Anotes—Torgan: nervous tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares placenta 8to9weeks 2NbHP8to9w"
/note="Organ: placenta; VecTor: pT7T3D (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI188862

427a12.x1 Soares placenta 8t09weeks 2NbHPBt09W Homo Sapiens CDNA clone IMAGE:1724926 3' similar to gb:X15414 ALDOSE REDUCTASE
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1099 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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46.3%; Score 19; DB 10; Length 294;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                 dev stage="Adult"
clone lib="NT0028"
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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GUINACY SEQUENCE.

GUINACY SEQUENCE.

TETRACHON NIGROVITICIS

TETRACHON NIGROVITICIS

BUKARYOTA: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii, Acanthopterygii; Percomorpha; Tetrachontoidea; Tetrachontoidea; Tetrachont.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Barnot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Bstimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note="Genoscope sequence ID : COAG253CA09SP1~end :
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100.0%; Pred. No. 21;
tive 0; Mismatches
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male testis"
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musculus cDNA clone 6030413B05 3' similar to U24166 Homo sapiens
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitacae; Vitis.

1 (bases 1 to 72)
Moser, C., Segala, C., Fontana, P., Salakhudtinov, I., Gatto, P.,
Pindo, M., Syprian, E., Toepfer, R., Grando, M.S. and Velasco, R.
Expressed sequence tags from different organs of Vitis vinifera
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Grape Bud pSPORT1 Library"
/note="Organ: bud; Vector: pSPORT1; Site_1: Not1; Site_2:
Sal1"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                      CF608248 12 bp mRNA linear BST 30-SEP-20 GEMMA01_001794 Grape Bud pSPORT1 Library Vitis vinifera cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: claudio.moser@ismaa.it
The sequencing work has been funded by the 'Fondazione Cassa di
Risparmio di Trento e Rovereto'
High quality sequence stop: 72.
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Laboratorio di Genetica Molecolare
Istituto Agrario di San Michele all'Adige (IASMA)
via E. Mach 1, San Michele all'Adige (TN), I-38010, Italia
Tel: 0039-0461-615314
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  Score 18; DB 29; Length 931;
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Pred. No. 54;
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100.0%; Pred. No. 22,
'... 0; Mismatches
Query Match
43.9%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches
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/dev_stage="bud_swelling"
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/cultivar="Pinot noir"
/db_xref="taxon:29760"
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CONTEXTIBLE OF DEPT STREET AND THE STREET S
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Fukuda, S., Eukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Saro, M., Sato, K., Shibata, X.,
Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Unpublished (1999)
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Okazaki,Y. Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone_lib="RIKEN full-length enriched, 13 days embryo
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/dev_stage="13 days_embryo"
/lab_host="DH10B"
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/clone="6030413B05"
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/strain="C57BL/6J"
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ACCESSION

KEYWORDS

VERSION

RESULT 6 AQ983222

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REFERENCE AUTHORS

COMMENT

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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building Map Building Cher_Gass. CITEL-2584D24.TF Cotter_Gass. CITEL-2584D24.TF Cotter_Gass. CITEL-2584D24.TF Cotter_Gass. CITEL-2584D24.TF Cotter_Cass. CITEL-2584D24.TF Cotter_Cass. CITEL-2584D24.TF Cotter_Cass. CITEL-2584D24.TF Cotter_Cass. CITEL-2584D24.TF Cotter_Cass. William Nierman, Mark Adams Department of Eukaryotic Genomics Research 712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0200 Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                              1 (bases 1 to 484)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="sperm"
/clone_lib="cirBl-Bl"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Callech Human BAC Library D"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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  AQ471300.
AQ471300.1 GI:4654954
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                                                                                  Homo sapiens (human)
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/lab host="DHIOB"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/clone lib="RpCI-23"
/clone lib="RpCI-23"
/clone lib="Rogan: Kidney Femals GS7BL/6J mouse kidney and/or BcoRI; Site 2: EcoRI; Female GS7BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACG3.6 vector at the EcoRI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                                                                               GSS 30-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akirret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M
Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.bufalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (lifo@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                         AQ983222
RPCI-23-307F19.TV RPCI-23 Mus musculus genomic clone
RPCI-23-307F19, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.5%; Score 17; DB 28; Length 408; 100.0%; Pred. No. 72; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1993)
Other GSSs: RPCI-23-307F19.TJ
Contact: Shaying Zara
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Pax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:10090"
'clone="RPCI-23-307F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 CTACATAACAACCACCT 397
                                                   182 GAATGAACTACATAACA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CTACATAACAACCACCT 24
                                                                                                                                                                                                                                                                      AQ983222
AQ983222.1 GI:6816427
GSS.
     GAATGAACTACATAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .408
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Matches 17; Conserve
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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FEATURES

RESULT

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ORIGIN

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Gaps

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWaPA2 (gilfyla) A132[A] A132[A] A132[A]. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          islibo4.bl WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clome_lib="WGS-ZmaysF (DHSa methyl filtered)" hote="Organ: immature ears; Site_1: Xba I; Site_2: Xba I; The vector was digested with Xba! Ind one nucleotide was added by fill in in the recessive 3' end. The genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
  /clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 569)
Rabinowicz,P.D. O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Katenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA

Fax: 516 367 8884
                                                                                      Laboratory Mouse DNA Resource
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/cultivar="B73"
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Location/Qualifiers
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Seq primer: -21M13UnivFwd
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/clone="ii81b04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'lab host="DH5a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 TTAGTCAGATACTACTT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC162058.1 GI:30188242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 TTAGTCAGATACTACTT 40
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Zea mays
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CC162058/c
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KEYWORDS
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Unpublished (2000)
Contact: Robert B. Weiss
Contact: Ob Utah
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dasses 1 to 567)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
           Tel: (206) 616-3618

Fax: (206) 616-3618

Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 3155 row: K column: 6
Seq primer: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ369484 1085 02-0CT-200 DNA linear GSS 02-0CT-200 1M0120P05F Mouse 108b plasmid UUGCIM library Mus musculus genomic clone UUGCIM0120P05 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.5%; Score 17; DB 28; Length 531;
100.0%; Pred. No. 75;
tive 0; Mismatches 0; Indels
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=1155 Col=6 Row=K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0120 row: P column: 05
Seg primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0120P05"
                                                                                                                                                                                                                                     High quality sequence stop: 531.
Location/Qualifiers
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                               Class: BAC ends
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SOURCE
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                                                                                                                                                                                                                                                                                                                                              EST 01-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
                                                                                                                                                                                                                                                                                                                                        CF207448
CAB20001_IVa_Ra_A09 Cabernet Sauvignon Flower bloom - CAB2 Vitis vinifera CDNA clone CAB20001_IVa_Ra_A09 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages Unpublished (2003)
Contact: Douglas Cook, PhD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            size-selected to contain the 0.5-3 kb size fraction."
                                                                                                                                                                            Gaps
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Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Jones,K. and Cook,D.
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0
                                                                                                                                    Score 17; DB 28; Length 569;
Pred. No. 76;
                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
                                                                                                              Query Match
41.5%; Score 17; ub.
Best Local Similarity 100.0%; Pred. No. 76;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Vitis vinifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616,
Tel: 530 754 6561
Fax: 530 754 6617
Email: droook@ucdavis.edu
Seg primer: GCCAAACGAAIGGTTAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   CF207448.1 GI:33401821
                                                                                                                                                                                                                                                 56 ACTACATAACAACCACC 40
                                                                                                                                                                                                             7 ACTACATAACAACCACC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAES Genome Facility
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/lone lib="QG EFGHJ lettuce serriola"
/clone lib="QG EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5, and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations ande with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG TISSUE=flowers environmental stress
TAG_LIB=CGEARIGCGGG"
TAG_SEGHJ lettuce serriola
                                                                                                                                                                                                                                        QGG17C07.yg.abl QG_EFCHJ lettuce serriola Lactuca sativa cDNA clone QGG17C07, mRNA sequence.
                                                                                                                                                                                                                          EST 22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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QG16A13.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QG16A13, mRNA sequence.
BQ874693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
Ellison,P., Kolkman,J., Slabaudh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Fmax: 1-(530)-752-9659
Fmax: 1-(540)-752-9659
Fmax: 1-(54
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                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://compgenomics.ucdavis.edu/
Unpublished (2002)
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/cultivar="L.serriola"
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100.0%; Pre
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132 AACTACATAACAACCAC 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cichorieae; Lactuca.
1 (bases 1 to 667)
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Best Local Similarity 100.
Matches 17; Conservative
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BQ997689
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0

Gaps

; 0

Query Match 41.5%; Score 17; DB 14; Length 649; Best Local Similarity 100.0%; Pred. No. 77; Matches 17; Conservative 0; Mismatches 0; Indels

6 AACTACATAACAACCAC 22

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/clone_lib="XGC-egg"
   Bennetzen, J.
Maize Genomics Consortium
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Sanger Institute
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1 (Dases 1 to 782)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                 Lactuca sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
                                                                                                                  Cichorieae; Lactuca.

1 (bases 1 to 695)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                    Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] singleton, see http://cgpdb.ucdavis.edu/ for details. Plate: QGI6 row: A column: 13.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                              Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Assundaton Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QG16A13"
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BQ874693.1 GI:22261253
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Best Local Similarity 100.(
Matches 17; Conservative
                                   Lactuca sativa
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BX783787

BX783787 XGC-egg Silurana tropicalis cDNA clone TEgg059102 3', mRNA
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TROPICALIS_SEQUENCE_ID: TEgg059102 q1kT7

Sequencing primer: T7

This sequence is from a Xenopus Gene Collection (XGC) library

CONSTINCT OUT ONNA was then ligated into pCS107 with EcoRI at the

EcoRINOLI CUT CUT CNNA was then ligated into pCS107 with EcoRI at the

S, end and NoLI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli XL1-blue.
                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="B73"
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/clone="ZNMBTa0661N17"
/clone="Lb="ZM 0.6 1.0 KB"
/note="Vector; PCT4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura; Mesobatrachia, Pipoldea; Pipidae,
Xenopodinae, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 870)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.5%; Score 17; DB 29; Length 782; 100.0%; Pred. No. 79; 0; Mismatches 0; Indels
                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silurana tropicalis (western clawed frog)
Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
                                                                                                                                                                                                       Seg primer: TF
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                   Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Unpublished (2003)
Other GSSs: PUJGG81TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX783787
BX783787.1 GI:39690993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ACTACATAACAACCACC 23
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/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from sug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
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ORIGIN

ö Query Match

41.5%; Score 17; DB 13; Length 870;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 17; Conservative 0; Mismatches 0; Indels

0; Gaps 21 ACCTTAGTCAGATACTA 37

287 ACCTTAGTCAGATACTA 303

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Search completed: March 25, 2004, 03:06:30 Job time : 2014 secs